

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-17
Perfect score: 11
Sequence: 1 AKKEKPNKPND 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
	1	11	100.0	11	3 AAY88545	Aay88545 NCAM Igl
	2	11	100.0	11	5 ABG69345	Abg69345 Human neu
	3	4	36.4	11	2 AAR49995	Aar49995 Mouse OSF
	4	4	36.4	11	3 AAY88528	Aay88528 NCAM Igl
	5	4	36.4	11	3 AAY88561	Aay88561 NCAM Igl
	6	4	36.4	11	4 ABP14934	Abp14934 HIV A03 s
	7	4	36.4	11	4 ABP21472	Abp21472 HIV A03 m
	8	4	36.4	11	4 ABP11867	Abp11867 HIV A01 s
	9	4	36.4	11	4 ABP13905	Abp13905 HIV A02 s

10	4	36.4	11	4	ABP13906	Abp13906	HIV A02 s
11	4	36.4	11	4	ABP13907	Abp13907	HIV A02 s
12	4	36.4	11	4	ABP16339	Abp16339	HIV A24 s
13	4	36.4	11	4	ABP19267	Abp19267	HIV B62 s
14	4	36.4	11	4	ABP19169	Abp19169	HIV B62 s
15	4	36.4	11	4	ABP23397	Abp23397	HIV A11 m
16	4	36.4	11	4	ABP19088	Abp19088	HIV B62 s
17	4	36.4	11	4	ABP21292	Abp21292	HIV A03 m
18	4	36.4	11	5	ABB74590	Abb74590	Transcrip
19	4	36.4	11	5	ABB74473	Abb74473	DNA repai
20	4	36.4	11	5	ABG69330	Abg69330	Human neu
21	4	36.4	11	7	ADC56785	Adc56785	Peptide (
22	3	27.3	11	1	AAP70892	Aap70892	Sequence
23	3	27.3	11	1	AAP82338	Aap82338	Compound
24	3	27.3	11	1	AAP82813	Aap82813	Peptide f
25	3	27.3	11	2	AAR08092	Aar08092	Antifreez
26	3	27.3	11	2	AAR27233	Aar27233	Thrombin
27	3	27.3	11	2	AAR36909	Aar36909	Insulin-l
28	3	27.3	11	2	AAR35381	Aar35381	Amphiphil
29	3	27.3	11	2	AAR43417	Aar43417	La/SSb ep
30	3	27.3	11	2	AAR33973	Aar33973	Amphiphil
31	3	27.3	11	2	AAR31163	Aar31163	C-termina
32	3	27.3	11	2	AAR34249	Aar34249	Mutant HT
33	3	27.3	11	2	AAR34247	Aar34247	Mutant HT
34	3	27.3	11	2	AAR34255	Aar34255	Mutant HT
35	3	27.3	11	2	AAR34257	Aar34257	Mutant HT
36	3	27.3	11	2	AAR34256	Aar34256	Mutant HT
37	3	27.3	11	2	AAR34254	Aar34254	Mutant HT
38	3	27.3	11	2	AAR34248	Aar34248	Mutant HT
39	3	27.3	11	2	AAR34253	Aar34253	Mutant HT
40	3	27.3	11	2	AAR34246	Aar34246	HTLV-I re
41	3	27.3	11	2	AAR41495	Aar41495	TNF inhib
42	3	27.3	11	2	AAR43603	Aar43603	Peptide d
43	3	27.3	11	2	AAR44562	Aar44562	Encoded b
44	3	27.3	11	2	AAR44561	Aar44561	Encoded b
45	3	27.3	11	2	AAR45132	Aar45132	Amphiphil
46	3	27.3	11	2	AAR32183	Aar32183	Ranakinin
47	3	27.3	11	2	AAR55163	Aar55163	Fragment
48	3	27.3	11	2	AAR67115	Aar67115	Anti-infl
49	3	27.3	11	2	AAR67036	Aar67036	Chemotact
50	3	27.3	11	2	AAR50563	Aar50563	Amphiphil
51	3	27.3	11	2	AAR55987	Aar55987	Ion chann
52	3	27.3	11	2	AAR59065	Aar59065	Cancer tr
53	3	27.3	11	2	AAR71762	Aar71762	Neurotens
54	3	27.3	11	2	AAR71761	Aar71761	Neurotens
55	3	27.3	11	2	AAR56948	Aar56948	Peptide w
56	3	27.3	11	2	AAR50448	Aar50448	Amphiphil
57	3	27.3	11	2	AAR82716	Aar82716	Shrimp tr
58	3	27.3	11	2	AAW21220	Aaw21220	Farnesyl
59	3	27.3	11	2	AAR76917	Aar76917	Thymosin
60	3	27.3	11	2	AAR78790	Aar78790	Rac1 (127
61	3	27.3	11	2	AAR86397	Aar86397	Soybean-d
62	3	27.3	11	2	AAR90259	Aar90259	Ion-chann
63	3	27.3	11	2	AAR91788	Aar91788	Ion-chann
64	3	27.3	11	2	AAR91787	Aar91787	Ion-chann
65	3	27.3	11	2	AAR92106	Aar92106	Human RIZ
66	3	27.3	11	2	AAR92105	Aar92105	Rat RIZ c

67	3	27.3	11	2	AAR85318	Aar85318	Human ret
68	3	27.3	11	2	AAW18499	Aaw18499	Amino-ter
69	3	27.3	11	2	AAW24438	Aaw24438	Nucleic a
70	3	27.3	11	2	AAW35836	Aaw35836	Soymetide
71	3	27.3	11	2	AAW09909	Aaw09909	Prostate
72	3	27.3	11	2	AAW04613	Aaw04613	Physalaem
73	3	27.3	11	2	AAW35540	Aaw35540	Biotin-la
74	3	27.3	11	2	AAW35543	Aaw35543	Immunizat
75	3	27.3	11	2	AAW83278	Aaw83278	NPF motif
76	3	27.3	11	2	AAW29629	Aaw29629	Peptide G
77	3	27.3	11	2	AAW29630	Aaw29630	Peptide G
78	3	27.3	11	2	AAW62116	Aaw62116	Human MDM
79	3	27.3	11	2	AAW66523	Aaw66523	Amphiphil
80	3	27.3	11	2	AAW48280	Aaw48280	Tyrosylpe
81	3	27.3	11	2	AAW65447	Aaw65447	Lebetin d
82	3	27.3	11	2	AAW45430	Aay45430	Immunogen
83	3	27.3	11	2	AAW03664	Aay03664	Amino aci
84	3	27.3	11	2	AAW06247	Aay06247	Staphyloc
85	3	27.3	11	2	AAW33736	Aay33736	Thrombin
86	3	27.3	11	2	AAW67760	Aaw67760	Platelet
87	3	27.3	11	2	AAW67757	Aaw67757	Platelet
88	3	27.3	11	2	AAW81004	Aaw81004	S. cerevi
89	3	27.3	11	2	AAW10761	Aay10761	Peptide u
90	3	27.3	11	2	AAW10750	Aay10750	Peptide u
91	3	27.3	11	2	AAW10762	Aay10762	Peptide u
92	3	27.3	11	3	AAB23898	Aab23898	Artificia
93	3	27.3	11	3	AAW88564	Aay88564	NCAM Igl
94	3	27.3	11	3	AAW88548	Aay88548	NCAM Igl
95	3	27.3	11	3	AAW88558	Aay88558	NCAM Igl
96	3	27.3	11	3	AAB12031	Aab12031	Cr2 motif
97	3	27.3	11	3	AAB12105	Aab12105	Rat RIZ p
98	3	27.3	11	3	AAB32196	Aab32196	Peptide m
99	3	27.3	11	3	AAW51238	Aay51238	C. roseus
100	3	27.3	11	3	AAB30392	Aab30392	Vaccinia

ALIGNMENTS

RESULT 1

AAW88545

ID AAW88545 standard; peptide; 11 AA.

XX

AC AAW88545;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #17.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKEKPNKPND 11
|||||||
Db 1 AKKEKPNKPND 11

RESULT 2

ABG69345

ID ABG69345 standard; peptide; 11 AA.

XX

AC ABG69345;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #17.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,

PT in the preparation of medicament for preventing death of cells presenting

PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which

CC comprises at least 5 contiguous amino acid residues of a sequence of the

CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,

CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 CC of a medicament for preventing death of cells presenting the NCAM or an
 CC NCAM ligand. The medicament is for the stimulation of the survival of
 CC heart muscle cells, such as survival after acute myocardial infarction.
 CC The medicament is for the treatment of diseases or conditions of the
 CC central and peripheral nervous system, such as postoperative nerve
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases or conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKEKPNKPND 11
 |||||
 Db 1 AKKEKPNKPND 11

RESULT 3

AAR49995

ID AAR49995 standard; protein; 11 AA.

XX

AC AAR49995;

XX

DT 25-MAR-2003 (revised)

DT 23-SEP-1994 (first entry)

XX

DE Mouse OSF-5 antigenic peptide 116-126.

XX

KW Mouse OSF-5; bone-related carboxypeptidase-like protein; growth factor;

KW adhesion molecule; osteogenesis; bone induction;

KW bone metabolism disorder; osteoporosis; osteopetrosis; Paget's disease;

KW antigen; immunogen; detection.

XX

OS Synthetic.

XX

PN EP588118-A2.

XX

PD 23-MAR-1994.

XX

PF 25-AUG-1993; 93EP-00113604.

XX

PR 28-AUG-1992; 92JP-00230029.

PR 03-DEC-1992; 92JP-00324033.

XX

PA (FARH) HOECHST JAPAN LTD.
 PA (HMRI) HOECHST MARION ROUSSELL LTD.
 XX
 PI Kawai S, Takeshita S, Okazaki M, Amann E;
 XX
 DR WPI; 1994-093794/12.
 XX
 PT New bone-related carboxy:peptidase OSF-5 - used to obtain prods. for the
 PT diagnosis and treatment of bone metabolic diseases, e.g. osteoporosis, or
 PT Paget's disease.
 XX
 PS Example 5; Page 6; 26pp; English.
 XX
 CC OSF-5 is a bone-specific carboxypeptidase which acts as an adhesion
 CC molecule or growth factor; it takes part in osteogenesis at the site of
 CC bone induction. OSF-5 can be used to treat bone metabolic diseases, e.g.
 CC osteoporosis, Paget's disease, osteomalacia, hyperostosis or
 CC osteopetrosis. To prepare anti-OSF-5 antibodies, five peptides (see
 CC AAR49995-R49999) corresponding to regions of the full-length mouse OSF-5
 CC sequence (AAR49994) were synthesised. Antisera raised against the
 CC peptides could be used to immunohistochemically search for the presence
 CC of OSF-5 in systemic slices from newborn mice and to detect expression of
 CC OSF-5 in E.coli, yeast and animal cells. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEKP 6
 ||||
 Db 3 KEKP 6

RESULT 4

AAAY88528

ID AAY88528 standard; peptide; 11 AA.

XX

AC AAY88528;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide D3.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX
 PF 23-SEP-1999; 99WO-DK000500.
 XX
 PR 29-SEP-1998; 98DK-00001232.
 PR 29-APR-1999; 99DK-00000592.
 XX
 PA (RONN/) RONN L C B.
 PA (BOCK/) BOCK E.
 PA (HOLM/) HOLM A.
 PA (OLSE/) OLSEN M.
 PA (OSTE/) OSTERGAARD S.
 PA (JENS/) JENSEN P H.
 PA (POUL/) POULSEN F M.
 PA (SORO/) SOROKA V.
 PA (RALE/) RALETS I.
 PA (BERE/) BEREZIN V.
 XX
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;
 XX
 DR WPI; 2000-293111/25.
 XX
 PT Compositions that bind neural cell adhesion molecules useful for treating
 PT disorders of the nervous system and muscles e.g. Alzheimer's and
 PT Parkinson's diseases.
 XX
 PS Claim 20; Page 82; 119pp; English.
 XX
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 CC NCAM is found in three forms, two of which are transmembrane forms, while
 CC the third is attached via a lipid anchor to the cell membrane. All three
 CC NCAM forms have an extracellular structure consisting five immunoglobulin
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
 CC terminal. The present sequence represents a peptide which binds to the
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
 CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
 CC outgrowth from NCAM presenting cells, and is also capable of promoting
 CC the proliferation of NCAM presenting cells. The compound may be used in
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.
 CC The compound may in particular be used to treat diseases of the central
 CC and peripheral nervous systems such as post operative nerve damage,
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 CC dementias, sclerosis, nerve degeneration associated with diabetes
 CC mellitus, disorders affecting the circadian clock or neuro-muscular
 CC transmission and schizophrenia. Conditions affecting the muscles may also
 CC be treated with the compound, such as conditions associated with impaired
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
 CC liver and bowel may also be treated using the compound. The compound is
 CC used in a prosthetic nerve guide, and also to stimulate the ability to
 CC learn, and to stimulate the memory of a subject
 XX
 SQ Sequence 11 AA;

Query Match

36.4%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
||||
Db 1 AKKE 4

RESULT 5

AAAY88561

ID AAY88561 standard; peptide; 11 AA.

XX

AC AAY88561;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide D3 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating

PT disorders of the nervous system and muscles e.g. Alzheimer's and

PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
||||
Db 1 AKKE 4

RESULT 6

ABP14934

ID ABP14934 standard; peptide; 11 AA.

XX

AC ABP14934;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 super motif pol peptide #308.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 174; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 8 KKEK 11

RESULT 7
 ABP21472
 ID ABP21472 standard; peptide; 11 AA.
 XX

AC ABP21472;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif pol peptide #467.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 309; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
| | | |
Db 8 KKEK 11

RESULT 8

ABP11867

ID ABP11867 standard; peptide; 11 AA.

XX

AC ABP11867;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A01 super motif pol peptide #139.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 112; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
| | | |
Db 3 KKEK 6

RESULT 9

ABP13905

ID ABP13905 standard; peptide; 11 AA.

XX

AC ABP13905;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif pol peptide #820.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 153; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5

||||

Db 7 KKEK 10

RESULT 10

ABP13906

ID ABP13906 standard; peptide; 11 AA.

XX

AC ABP13906;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif pol peptide #821.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 153; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 5 KKEK 8

RESULT 11
 ABP13907
 ID ABP13907 standard; peptide; 11 AA.
 XX
 AC ABP13907;

XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A02 super motif pol peptide #822.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 153; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
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 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
||||
Db 4 KKEK 7

RESULT 12

ABP16339

ID ABP16339 standard; peptide; 11 AA.

XX

AC ABP16339;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A24 super motif pol peptide #519.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 203; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 3 KKEK 6

RESULT 13

ABP19267

ID ABP19267 standard; peptide; 11 AA.

XX

AC ABP19267;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B62 super motif pol peptide #273.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX
 PS Claim 32; Page 263; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 7 KKEK 10

RESULT 14
 ABP19169
 ID ABP19169 standard; peptide; 11 AA.
 XX
 AC ABP19169;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B62 super motif pol peptide #175.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.

XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 261; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 3 KKEK 6

RESULT 15
 ABP23397
 ID ABP23397 standard; peptide; 11 AA.
 XX
 AC ABP23397;
 XX

DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV All motif pol peptide #339.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 348; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match

36.4%; Score 4; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
|||
Db 8 KKEK 11

RESULT 16

ABP19088

ID ABP19088 standard; peptide; 11 AA.

XX

AC ABP19088;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B62 super motif pol peptide #94.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 260; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 3 KKEK 6

RESULT 17

ABP21292

ID ABP21292 standard; peptide; 11 AA.

XX

AC ABP21292;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A03 motif pol peptide #287.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 305; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
| | | |
Db 4 KKEK 7

RESULT 18

ABB74590

ID ABB74590 standard; peptide; 11 AA.

XX

AC ABB74590;

XX

DT 18-APR-2002 (first entry)

XX

DE Transcription factor nuclear localisation signal peptide SEQ ID NO:354.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.

XX

OS Homo sapiens.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.

XX

PS Claim 14; Page 76; 107pp; English.

XX

CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5

||||

Db 7 KKEK 10

RESULT 19

ABB74473

ID ABB74473 standard; peptide; 11 AA.

XX

AC ABB74473;

XX

DT 18-APR-2002 (first entry)

XX

DE DNA repair protein nuclear localisation signal peptide SEQ ID NO:237.
XX
KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
OS Eukaryota.
XX
PN WO200193836-A2.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018657.
XX
PR 09-JUN-2000; 2000US-0210925P.
XX
PA (BOUL/) BOULIKAS T.
XX
PI Boulikas T;
XX
DR WPI; 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 69; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
Db 7 KKEK 10

RESULT 20

ABG69330

ID ABG69330 standard; peptide; 11 AA.

XX

AC ABG69330;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #2.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Claim 26; Page 39; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells
CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve

CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases of conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
 ||||
 Db 1 AKKE 4

RESULT 21

ADC56785

ID ADC56785 standard; peptide; 11 AA.

XX

AC ADC56785;

XX

DT 18-DEC-2003 (first entry)

XX

DE Peptide (SeqID 5) derived from the human HMG-2 protein.

XX

KW antibody; high mobility group protein-1; HMG-1; HMG-2; peptide immunogen;

KW MD78; sepsis; human.

XX

OS Homo sapiens.

XX

PN JP2003096099-A.

XX

PD 03-APR-2003.

XX

PF 10-JUL-2002; 2002JP-00200946.

XX

PR 13-JUL-2001; 2001JP-00213997.

XX

PA (SHIN-) SHINOTEST KK.

XX

DR WPI; 2003-572672/54.

XX

PT New antibody for measuring human high mobility group protein-1 (HMG-1)

PT binds human HMG-1, but does not bind human HMG-2 protein.

XX

PS Example 1; SEQ ID NO 5; 28pp; Japanese.

XX

CC This invention relates to a novel antibody which specifically binds human

CC high mobility group protein-1 (HMG-1) and which does not bind with human
CC HMG-2 protein. Specifically, it relates to an immunological reagent for
CC measuring human HMG-1 in a sample comprising the new antibody. The
CC peptide immunogen may be modified from the defined sequence by the
CC deletion, substitution, addition, or modification of one or more
CC residues. A hybridoma expressing the new antibody is designated MD78. HMG
CC -1 may be used as a marker of disease such as sepsis and the antibody and
CC method may be useful for example in clinical laboratory tests.
CC Measurement of human HMG using the new antibody is easier and more
CC reliable than with current methods, furthermore the method may be
CC automated. This peptide sequence is a human peptide (SeqID 5) derived
CC from the human HMG-2 protein sequence in an exemplification of the
CC invention.

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNKP 9

||||

Db 5 PNKP 8

RESULT 22

AAP70892

ID AAP70892 standard; peptide; 11 AA.

XX

AC AAP70892;

XX

DT 31-OCT-2002 (revised)

DT 05-JUN-1991 (first entry)

XX

DE Sequence of analogue of serine protease inhibitor.

XX

KW Enzyme; complement activation; therapy; clot degradation.

XX

OS Synthetic.

XX

PN EP238473-A.

XX

PD 23-SEP-1987.

XX

PF 17-MAR-1987; 87EP-00870035.

XX

PR 18-MAR-1986; 86US-00840810.

PR 06-FEB-1987; 87US-00006725.

XX

PA (MONS) MONSANTO CO.

XX

PI Glover GI, Schasteen CS;

XX

DR WPI; 1987-265792/38.

XX

PT New peptide cpds. which inhibit serine protease - extensively homologous
PT with natural inhibitors, useful e.g. for treating excessive complement

PT activation.
XX
PS Claim 26; Page 31; 34pp; English.
XX
CC The peptides of the invention are useful for treating diseases associated
CC with excessive protease activity particularly those involved in
CC complement activation, blood clotting and clot degradation. The usual
CC dose is 0.1-10mg/kg. (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 4 NKP 6

RESULT 23

AAP82338

ID AAP82338 standard; protein; 11 AA.

XX

AC AAP82338;

XX

DT 13-NOV-1990 (first entry)

XX

DE Compound in vaccine against Plasmodium falciparum malaria (Formula III).

XX

KW Malaria vaccines; polymers; Plasmodium falciparum; asexual blood stage;
KW human parasite.

XX

OS Synthetic.

XX

PN EP275196-A.

XX

PD 20-JUL-1988.

XX

PF 13-JAN-1988; 88EP-00300262.

XX

PR 14-JAN-1987; 87US-00003194.

PR 29-DEC-1987; 87US-00135027.

XX

PA (PATA/) PATARROYO M E.

XX

PI Patarroyo ME;

XX

DR WPI; 1988-199632/29.

XX

PT New peptide(s) and peptide polymers - useful for prodn. of malaria
PT vaccines.

XX

PS Claim 15 (III); Page 13; 13pp; English.

XX

CC The peptide is a vaccine component against the asexual blood stage of the
CC malaria parasite. It is the synthetic hybrid protein SPf 83.1 peptide of

CC 11 amino acids. It corresponds to residues 43-536 of the 195 kD sequence
CC described by Holder et al. Nature, Vol.317, pages 270-273. Sep.1985. The
CC peptide is an alpha hydrophilic structure, and the compound even on its
CC own elicits antibodies delaying the appearance of parasitaemia in some
CC vaccinated animals. Mixtures of the peptides of AAP82336-P82340 provide
CC complete immunity

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5

|||

Db 6 KEK 8

RESULT 24

AAP82813

ID AAP82813 standard; protein; 11 AA.

XX

AC AAP82813;

XX

DT 06-DEC-1990 (first entry)

XX

DE Peptide fragment of Plasmodium proteins used in antimalaria vaccines.

XX

KW Plasmodium; antimalarial vaccine; parasite.

XX

OS Synthetic.

XX

PN US4735799-A.

XX

PD 05-APR-1988.

XX

PF 14-JAN-1987; 87US-00003194.

XX

PR 29-DEC-1987; 87US-00135027.

XX

PA (PATA/) PATARROYO M E.

XX

PI Patarroyo ME;

XX

DR WPI; 1988-112448/16.

XX

PT New peptide fragments of Plasmodium proteins - useful for prodn. of
PT antimalarial vaccines.

XX

PS Claim 3; Page 9; 6pp; English.

XX

CC This peptide is an alpha hydrophilic structure corresponding to amino
CC acid residues 43-53 of the 195 kD amino acid sequence. (Holder et al.
CC Nature, Vol. 317, pages 270-273, September 1985). Vaccines contain (I),
CC (II) and (III); AAP82811, AAP82812 and AAP82812 resp; in a wt. ratio of
CC (1-10):(1-10):(1-10), esp. 1:1:1, in normal saline soln. or squalene.
CC Immunogenic activity may be increased by coupling (I)-(III) to bovine

CC serum albumin with gluteraldehyde or by coupling (I)-(III) by
CC copolymerisation. The peptides (I)-(V); AAP82811-15; provide partial
CC immunity to malaria caused by Plasmodium falciparum. Combinations of (I)-
CC (III) provide complete immunity in Aotos monkeys

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5

|||

Db 6 KEK 8

RESULT 25

AAR08092

ID AAR08092 standard; protein; 11 AA.

XX

AC AAR08092;

XX

DT 25-MAR-2003 (revised)

DT 01-MAR-1991 (first entry)

XX

DE Antifreeze segment #2 encoded by SS3.

XX

KW synthetic antifreeze polypeptide; cryopreservation;

KW core repetitive sequence.

XX

OS Synthetic.

XX

PN WO9013571-A.

XX

PD 15-NOV-1990.

XX

PF 10-MAY-1989; 89US-00350481.

XX

PR 10-MAY-1989; 89US-00350481.

PR 10-APR-1990; 90US-00507716.

XX

PA (DNAP) DNA PLANT TECHN COR.

XX

PI Warren GJ, Mueller JM, Mckown RJ, Dunsmuir P;

XX

DR WPI; 1990-361428/48.

XX

PT New anti-freeze poly-peptide(s) - used for cryo-protection of e.g. foods,

PT medically used biological(s), plant prods. or plants during growth.

XX

PS Disclosure; Fig 4; 11lpp; English.

XX

CC Synthetic anti-freeze polypeptides (saf) comprise a specifically
CC cleavable site and a region containing at least two "core" segments such
CC as the 11mer given here. The saf's suppress ice crystal growth by binding
CC to the growing crystal face and blocking sites for further crystal
CC growth. They can be used to maximise retention of important properties of

CC organic materials through freezing and thawing processes. The basic
CC design of the polypeptides is based on known antifreeze polypeptides from
CC insects and fish, e.g. the winter flounder. See also AAQ06649-Q06652,
CC AAQ06656, AAQ06658, AAQ06660-Q06672, AAR08070-6, AAR08087-R08091,
CC AAR08093. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 8 AKK 10

RESULT 26

AAR27233

ID AAR27233 standard; peptide; 11 AA.

XX

AC AAR27233;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX

DE Thrombin receptor agonist peptide.

XX

KW Diagnosis; cardiovascular disease; wound healing; restenosis; thrombosis;

KW unstable angina treatment; myocardial infarction; thrombotic;

KW thromboembolytic stroke.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_site 3

FT /note= "cyclohexylalanine"

FT modified_site 4

FT /note= "cyclohexylalanine"

XX

PN WO9214750-A1.

XX

PD 03-SEP-1992.

XX

PF 19-FEB-1992; 92WO-US001312.

XX

PR 19-FEB-1991; 91US-00657769.

PR 07-NOV-1991; 91US-00789184.

XX

PA (REGC) UNIV CALIFORNIA.

PA (CORT-) COR THERAPEUTICS INC.

XX

PI Coughlin SR, Scarborough RM;

XX

DR WPI; 1992-316119/38.

XX
PT DNA encoding cell surface receptor for thrombin - useful for determining
PT thrombin in diagnosing e.g. cardiovascular diseases, also to treat wound
PT healing, restenosis etc.
XX
PS Claim 10; Page 59; 81pp; English.
XX
CC The peptide is a thrombin receptor agonist and can be used in a
CC pharmaceutical compsn. for wound healing. It is also useful in
CC encouraging platelet aggregation, e.g. in localised application at
CC internal bleeding sites of haemophiliacs, and in mimicking thrombin's
CC ability to stimulate fibroblast proliferation to promote wound healing.
CC See also AAR27224-R27240. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
| | |
Db 8 PND 10

RESULT 27

AAR36909

ID AAR36909 standard; peptide; 11 AA.

XX

AC AAR36909;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;
KW injury; ageing; disease; photodegeneration; trauma; axotomy;
KW neurotoxic-excitatory degeneration; diabetic retinopathy;
KW ischemic neuronal degeneration; inherited retinal dystrophy;
KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;
KW ceroid-lipofuscosis; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1. .11

XX

PN WO9308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.

XX

PR 08-NOV-1991; 91US-00790690.

PR 15-OCT-1992; 92US-00963329.

XX

PA (CEPH-) CEPHALON INC.
 XX
 PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;
 XX
 DR WPI; 1993-167389/20.
 XX
 PT Use of IGF-I or IGF-II or their functional derivs. - for treating
 PT disorders characterised by death and/or dysfunction of retinal cells.
 XX
 PS Example; Page 71; 97pp; English.
 XX
 CC The sequence is that of a functional derivative of human insulin-like
 CC growth factor (IGF)-II which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosis or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||
 Db 4 NKP 6

RESULT 28

AAR35381

ID AAR35381 standard; peptide; 11 AA.

XX

AC AAR35381;

XX

DT 25-MAR-2003 (revised)

DT 07-JUN-1993 (first entry)

XX

DE Amphiphilic peptide #112 used to treat oral infections.

XX

KW Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;

KW anti-fungal; dental plaque; dental caries; periodontal disease;

KW gingivitis; ionophore; ion-channel forming.

XX

OS Synthetic.

XX

PN W09301723-A1.

XX

PD 04-FEB-1993.

XX

PF 09-JUL-1992; 92WO-US005757.

XX

PR 25-JUL-1991; 91US-00735070.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Berkowitz B, Jacob L;

XX

DR WPI; 1993-058434/07.

XX

PT Peptide(s) for prophylaxis and treatment of oral disorders - used for
PT periodontal disease, plaque, dental caries, gingivitis, etc.

XX

PS Claim 2; Page 129; 143pp; English.

XX

CC This is a specific example of a highly generic formula covering preferred
CC amphiphilic peptides for use in preventing or treating adverse oral
CC conditions. The peptide is an ionophore (i.e. an ion- channel forming
CC peptide) which has anti-bacterial, anti-viral, anti- fungal activity,
CC etc. making it suitable for use in oral compositions to treat or prevent
CC periodontal disease, plaque, dental caries, halitosis and gingivitis. The
CC anti-bacterial action will also be useful against bacteria associated
CC with dental implant infections and the peptides can stimulate the healing
CC of wounds in the oral cavity. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 29

AAR43417

ID AAR43417 standard; peptide; 11 AA.

XX

AC AAR43417;

XX

DT 25-MAR-2003 (revised)

DT 12-MAY-1994 (first entry)

XX

DE La/SSb epitope 270.

XX

KW Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;

KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;

KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';

KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.

XX

OS Homo sapiens.

XX

PN W09321223-A1.

XX

PD 28-OCT-1993.

XX

PF 13-APR-1993; 93WO-US003484.

XX

PR 13-APR-1992; 92US-00867819.

XX

PA (OKLA) UNIV OKLAHOMA STATE.

XX

PI Harley JB;

XX

DR WPI; 1993-351658/44.

XX

PT New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB
PT and Sm B/B' antigens and ribo:nucleoprotein, used for diagnosing and
PT treating auto-immune disorders e.g. systemic lupus erythematosus.

XX

PS Claim 1; Page 30; 43pp; English.

XX

CC The sequences given in AAR43391-562 are linear epitopes which are derived
CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear
CC ribonucleoprotein (nRNP) and the Sm B/B' polypeptide. These antigens are
CC common in systemic lupus erythematosus (SLE) and closely related
CC disorders. The Ro/SSA family of proteins has been shown to have several
CC molecular forms which are defined by the molecular weight of the antigen
CC identified. The major form has a molecular weight of 60 kD and two
CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a
CC member of this group of autoantibodies and binds small RNAs with a
CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA
CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD
CC monomeric phosphoprotein which associates with RNA polymerase III
CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,
CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F
CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for
CC preventing, treating or screening autoimmune disorders, especially SLE or
CC Sjogrens syndrome (SS). They bind to a human autoantibody and may
CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5

|||

Db 7 KEK 9

RESULT 30

AAR33973

ID AAR33973 standard; peptide; 11 AA.

XX

AC AAR33973;

XX

DT 25-MAR-2003 (revised)

DT 21-JUL-1993 (first entry)

XX

DE Amphiphilic peptide (e), #2.

XX

KW Hydrophobic; hydrophilic; neutral; (e); ionophore; channel-forming;
KW human; virus; antimicrobial; antiviral; antibacterial; antitumour;
KW antiparasitic; spermicide; preservative; sterilant; disinfectant;
KW wound healing; burn; infection; eye; cysts; spores; trophozoites; plants;
KW contamination.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note= "May be acetylated"
FT	Modified-site	11
FT		/note= "May be amidated"

XX

PN WO9305802-A1.

XX

PD 01-APR-1993.

XX

PF 04-SEP-1992; 92WO-US007622.

XX

PR 13-SEP-1991; 91US-00760054.

PR 20-APR-1992; 92US-00870960.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP, Williams JI;

XX

DR WPI; 1993-117245/14.

XX

PT New biologically active amphiphilic peptide cpds. - having ion channel-
PT forming properties used for inhibiting growth of target cells, virus or
PT viral-infected cells.

XX

PS Claim 27; Page 33; 46pp; English.

XX

CC This sequence is an example of a biologically active peptide which
CC corresponds to the generic sequence; R1-R2-R2-R1-R1-R2-R2-R1-R2-R1
CC where R1 = a hydrophobic amino acid; and R2 = a basic hydrophilic or
CC neutral hydrophilic amino acid. This basic structure was designated (e).
CC Peptides such as this are ionophores ie. they have channel-forming
CC properties. The peptides can be administered to a host, eg, humans, to
CC inhibit the growth of a target cell, virus or virally infected cell. They
CC can be used as antimicrobial, antiviral agents, antibacterial agents,
CC antitumour agents, antiparasitic agents, and as spermicides. They can be
CC used as preservatives or sterilants or disinfectants. These peptides can
CC also be used to promote or stimulate healing of wounds, to treat and/or
CC prevent prevent skin or burn infections, to prevent or treat eye
CC infections and to kill cysts, spores or trophozoites of infection causing
CC organisms. The peptides may also be administered to plants to prevent or
CC treat microbial, viral or parasitic contamination. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 31

AAR31163

ID AAR31163 standard; peptide; 11 AA.

XX

AC AAR31163;

XX

DT 25-MAR-2003 (revised)

DT 10-MAY-1993 (first entry)

XX

DE C-terminal substd. amphiphilic peptide #112.

XX

KW ion-channel forming; ionophore; antibiotic; anti-tumour; anti-virus;
KW wound healing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Leu-(C=O)-T, T= O-R, NH-NH2, NH-OH or NR'R''; R=
FT opt.substd. 1-10C aliphatic, aromatic or aralkyl gp.; R',
FT R''= H or from one of gps. i and ii; gp.i= 1-10C hydroxy-
FT substd. aliphatic, aromatic or aralkyl gp.; gp.ii= amino-
FT substd. aliphatic, aromatic, aralkyl or alkylaromatic gp.
FT and at least one of R' and R'' = gp.i or gp.ii''"

XX

PN WO9222317-A1.

XX

PD 23-DEC-1992.

XX

PF 01-JUN-1992; 92WO-US004603.

XX

PR 12-JUN-1991; 91US-00713716.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP;

XX

DR WPI; 1993-017904/02.

XX

PT New C-terminal-substd. amphiphilic peptide(s) - for treating bacterial,
PT viral or fungal infections and tumours, also useful as spermicide.

XX

PS Claim 21; Page 114; 124pp; English.

XX

CC This peptide is a preferred example of a highly generic amphiphilic
CC peptide with a C-terminal modification which increases the peptide's
CC biological activity c.f. the unmodified peptide. The preferred C-terminal
CC modification is -(CO)-NHCH2CH2OH or -(CO)-NHCH2CH2NH2. Such substd.
CC peptides may be used for inhibiting the growth of a target cell, virus or
CC virally-infected cell in a host. The peptides have a broad range of
CC potent antibiotic activity, e.g. against gram- negative and gram-positive

CC bacteria, fungi, protozoa and parasites. The peptides can also be used to
CC promote wound healing and treatment of burns. Other preferred amphiphilic
CC peptides include magainins and their analogues, PGLa, XPF, CPF, a
CC cecropin and a sarcotoxin. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 32

AAR34249

ID AAR34249 standard; peptide; 11 AA.

XX

AC AAR34249;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.3.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93

CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 33

AAR34247

ID AAR34247 standard; peptide; 11 AA.

XX

AC AAR34247;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.1.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7

|||

Db 4 KPN 6

RESULT 34

AAR34255

ID AAR34255 standard; peptide; 11 AA.

XX

AC AAR34255;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.9.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 35

AAR34257

ID AAR34257 standard; peptide; 11 AA.

XX

AC AAR34257;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.11.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-

CC 98 were required for absorption of neutralising anti-peptide antibodies

CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which

CC sequential amino acids were each replaced by the amino acid alanine.

CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native

CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93

CC and 95 were important for HTLV-I neutralisation. See also AAR34225-56.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 36

AAR34256

ID AAR34256 standard; peptide; 11 AA.

XX

AC AAR34256;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.10.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 37

AAR34254

ID AAR34254 standard; peptide; 11 AA.

XX

AC AAR34254;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.8.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7

Db |||
 4 KPN 6

RESULT 38

AAR34248

ID AAR34248 standard; peptide; 11 AA.

XX

AC AAR34248;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.2.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-

CC 98 were required for absorption of neutralising anti-peptide antibodies

CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which

CC sequential amino acids were each replaced by the amino acid alanine.

CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native

CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93

CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 2 AKK 4

RESULT 39

AAR34253

ID AAR34253 standard; peptide; 11 AA.

XX

AC AAR34253;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.7.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7

|||

Db 4 KPN 6

RESULT 40

AAR34246

ID AAR34246 standard; peptide; 11 AA.

XX

AC AAR34246;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE HTLV-I residues 88-98, peptide 2L-1.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN W09306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Palker TJ, Haynes BF;

XX

DR WPI; 1993-134125/16.

XX

PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX

PS Example 7; Page 32; 50pp; English.

XX

CC To determine which amino acids within the HTLV-I envelope amino acids 88-
 CC 98 were required for absorption of neutralising anti-peptide antibodies
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
 CC sequential amino acids were each replaced by the amino acid alanine.
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7

|||

Db 4 KPN 6

RESULT 41

AAR41495

ID AAR41495 standard; peptide; 11 AA.
 XX
 AC AAR41495;
 XX
 DT 23-FEB-1994 (first entry)
 XX
 DE TNF inhibitory peptide VII.
 XX
 KW Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.
 XX
 OS Synthetic.
 XX
 PN JP05194594-A.
 XX
 PD 03-AUG-1993.
 XX
 PF 21-JAN-1992; 92JP-00029044.
 XX
 PR 21-JAN-1992; 92JP-00029044.
 XX
 PA (SAGA) SAGAMI CHEM RES CENTRE.
 XX
 DR WPI; 1993-282916/36.
 XX
 PT TNF inhibitory novel peptide(s) - include N-terminal amino Gp. which is
 PT opt. modified with acetyl, T-butoxy-carbonyl or benzyl-oxy-carbonyl Gp.
 PT and C-terminal carboxy Gp. is opt. amidated.
 XX
 PS Claim 1; Page 6; 8pp; Japanese.
 XX
 CC The sequences given in AAR41489-99 are tumour necrosis factor (TNF)
 CC inhibitory peptides. They may optionally be modified at the N- terminal
 CC with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and at the C-
 CC terminal they are optionally amidated. These peptides are produced by
 CC solid phase synthesis methods and may be produced at low cost
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 3 AKK 5

RESULT 42

AAR43603

ID AAR43603 standard; peptide; 11 AA.
 XX
 AC AAR43603;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAY-1994 (first entry)
 XX
 DE Peptide derived from insulin-like growth factor.

XX
 KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;
 KW epilepsy; Parkinson's disease; head injury; spinal cord injury;
 KW age- related neuronal loss; amyotrophic lateral sclerosis; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .11
 XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 17; Page 80; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC neuronal cells in a mammal that are at risk of dying or to treat a head
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||
 Db 4 NKP 6

RESULT 43
 AAR44562
 ID AAR44562 standard; protein; 11 AA.
 XX
 AC AAR44562;
 XX

DT 25-MAR-2003 (revised)
 DT 26-MAY-1994 (first entry)
 XX
 DE Encoded by human Ews exon 9/Hum-Fli-1 exon 4 fusion.
 XX
 KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene;
 KW malignant melanoma; hum-fli-1;
 KW primitive peripheral neuroectodermal tumour; human chromosome 11;
 KW human chromosome 22.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .5
 FT /note= "encoded by 3'-end of Ews exon 9"
 FT Region 6. .11
 FT /note= "encoded by 5'-end of Hum-Fli-1 exon 4"
 XX
 PN W09323549-A2.
 XX
 PD 25-NOV-1993.
 XX
 PF 19-MAY-1993; 93WO-FR000494.
 XX
 PR 20-MAY-1992; 92FR-00006123.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Aurias A, Delattre O, Desmaze C, Melot T, Peter M, Plougastel B;
 PI Thomas G, Zucman J;
 XX
 DR WPI; 1993-386580/48.
 DR N-PSDB; AAQ50675.
 XX
 PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence
 PT involved in chromosomal trans-location, also derived mRNA, probes, fusion
 PT proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.
 XX
 PS Disclosure; Fig 14; 123pp; French.
 XX
 CC The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene
 CC have been sequenced (see AAQ50646 and AAQ50662, respectively). The
 CC different fusion products which could be formed by fusing exons from the
 CC two genes, as happens after specific chromosomal translocations, can be
 CC predicted. See AAR44558-R44565 for the amino acid sequences resulting
 CC from the different fusion events. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||
 Db 2 NKP 4

RESULT 44

AAR44561

ID AAR44561 standard; protein; 11 AA.

XX

AC AAR44561;

XX

DT 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX

DE Encoded by human Ews exon 9/Hum-Fli-1 exon 7 fusion.

XX

KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene;

KW malignant melanoma; hum-fli-1;

KW primitive peripheral neuroectodermal tumour; human chromosome 11;

KW human chromosome 22.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /note= "encoded by 3'-end of Ews exon 9"

FT Region 6. .11

FT /note= "encoded by 5'-end of Hum-Fli-1 exon 7"

XX

PN WO9323549-A2.

XX

PD 25-NOV-1993.

XX

PF 19-MAY-1993; 93WO-FR000494.

XX

PR 20-MAY-1992; 92FR-00006123.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Aurias A, Delattre O, Desmaze C, Melot T, Peter M, Plougastel B;

PI Thomas G, Zucman J;

XX

DR WPI; 1993-386580/48.

DR N-PSDB; AAQ50674.

XX

PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence

PT involved in chromosomal trans-location, also derived mRNA, probes, fusion

PT proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.

XX

PS Disclosure; Fig 14; 123pp; French.

XX

CC The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene

CC have been sequenced (see AAQ50646 and AAQ50662, respectively). The

CC different fusion products which could be formed by fusing exons from the

CC two genes, as happens after specific chromosomal translocations, can be

CC predicted. See AAR44558-R44565 for the amino acid sequences resulting

CC from the different fusion events. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 2 NKP 4

RESULT 45

AAR45132

ID AAR45132 standard; peptide; 11 AA.

XX

AC AAR45132;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1994 (first entry)

XX

DE Amphiphilic peptide for N-terminal lipophilic substitution.

XX

KW Ion channel; magainin; PGLa; XPF; CPF; cecropin; sarcotoxin; amphiphilic;
KW hydrophobic; hydrophilic; lipophilic; growth; inhibition; target cell;
KW virus; virally-infected cell; antimicrobial; antiviral; antitumour;
KW antiparasitic; spermicide; wound healing; burn; infection.

XX

OS Synthetic.

XX

PN WO9324138-A1.

XX

PD 09-DEC-1993.

XX

PF 27-MAY-1993; 93WO-US005192.

XX

PR 01-JUN-1992; 92US-00891201.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U;

XX

DR WPI; 1993-405419/50.

XX

PT Peptide(s) or proteins with an N-terminal lipophilic substit. - used for
PT inhibiting growth of target cell, virus or virally-infected cell.

XX

PS Disclosure; Page 97-103; 113pp; English.

XX

CC A novel compsn. for inhibiting growth of a target cell, virus or virally-
CC infected cell comprises a peptide of formula T-N(W)-X (I). X is a
CC biologically active amphiphilic ion channel-forming peptide or protein;
CC pref. a magainin peptide, a PGLa peptide, a XPF peptide, a CPF peptide, a
CC cecropin or a sarcotoxin. N is the nitrogen of the N-terminal amino
CC group. T is a lipophilic moiety; pref. R-CO, where R is a 2-16C
CC hydrocarbon (alkyl or aromatic or alkylaromatic). T is pref. an octanoyl
CC group. W is T or hydrogen. Amphiphilic peptides as examples of X are
CC given in AAR45115-138. The N-terminal substd. peptides and proteins have
CC increased biological activity as compared with unsubstd. peptides or

CC proteins or peptides substd. at the N-terminal with an acetyl gp. They
CC can be used as antimicrobial agents, antiviral agents, antitumour agents,
CC antiparasitic agents or spermicides and can also exhibit other bioactive
CC functions. They can also be used in promoting or stimulating wound
CC healing, for the treatment of external burns and to treat and/or prevent
CC skin and burn infections or eye infections. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 46

AAR32183

ID AAR32183 standard; peptide; 11 AA.

XX

AC AAR32183;

XX

DT 25-MAR-2003 (revised)

DT 04-JUN-1993 (first entry)

XX

DE Ranakinin.

XX

KW Substance P; dopaminergic neurone; NK-1 type receptor; neuropeptide;

KW tachykinin family; sub-family physalaemine; frog brain.

XX

OS Rana ridibunda.

XX

PN FR2677362-A1.

XX

PD 11-DEC-1992.

XX

PF 04-JUN-1991; 91FR-00006759.

XX

PR 04-JUN-1991; 91FR-00006759.

XX

PA (CNRS) CENT NAT RECH SCI.

PA (UYCR-) UNIV CREIGHTON.

XX

PI Vaudry H, Conlon JM;

XX

DR WPI; 1993-047140/06.

DR N-PSDB; AAQ36644.

XX

PT New tacykinin peptide derivs. e.g. ranakinin - as NK-1 agonists and

PT substance P analogues for treating arterial tension and inflammation.

XX

PS Claim 6; Page 24; 33pp; French.

XX

CC The neuropeptide ranakinin was isolated from extracts of brain from the

CC frog R. ridibunda by screening for reactivity with serum contg. antibodies
 CC to the C-terminal part of Substance P. A generic formula (AAR32182) for
 CC other tachykinin-like peptides was derived from ranakinin. Neuropeptides
 CC belonging to the tachykinin family act as NK-1 agonists and substance P
 CC analogues. The peptides corresponding to the generic formula, including
 CC ranakinin, are likely to have tachykinin-like properties, e.g.
 CC involvement in transmission of nociceptive information, in arterial
 CC pressure, salivation, smooth muscle contraction and regulation of
 CC dopaminergic transmission at the level of the nigro-striatal complex. See
 CC also AAQ36644. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
 |||
 Db 1 KPN 3

RESULT 47

AAR55163

ID AAR55163 standard; protein; 11 AA.

XX

AC AAR55163;

XX

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

XX

DE Fragment of retinoic acid receptor RAR-beta.

XX

KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;

KW retinoid; antibody.

XX

OS Homo sapiens.

XX

PN US5317090-A.

XX

PD 31-MAY-1994.

XX

PF 11-DEC-1992; 92US-00989902.

XX

PR 16-DEC-1987; 87US-00133687.

PR 17-DEC-1987; 87US-00134130.

PR 20-JUN-1988; 88US-00209009.

PR 30-NOV-1988; 88US-00278136.

PR 30-MAR-1989; 89US-00330405.

PR 21-AUG-1991; 91US-00751612.

PR 30-MAR-1992; 92US-00860577.

XX

PA (INSP) INST PASTEUR.

XX

PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;

PI Brand N, De The HB;

XX

DR WPI; 1994-176333/21.
 XX
 PT Antibody specific for retinoic acid receptor-beta - useful for detecting,
 PT quantifying and identifying agonists and antagonists of retinoid
 PT activity.
 XX
 PS Claim 4; Col 40; 35pp; English.
 XX
 CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.
 CC The hap gene is transcribed at low level in most human tissues, but the
 CC gene is overexpressed in prostate and kidney. Six out of seven hepatoma or
 CC hepatoma-derived cell lines express a small hap transcript which is
 CC undetectable in normal adult and foetal livers but present in all non-
 CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
 |||
 Db 7 KKE 9

RESULT 48

AAR67115

ID AAR67115 standard; peptide; 11 AA.

XX

AC AAR67115;

XX

DT 25-MAR-2003 (revised)

DT 30-JUN-1995 (first entry)

XX

DE Anti-inflammatory peptide (AIP-IL8R2) contg. proline brackets.

XX

KW anti-inflammatory peptide; interleukin-8 receptor; inhibitor; mimic;

KW interaction site; constrained conformation.

XX

OS Synthetic.

XX

PN WO9425482-A1.

XX

PD 10-NOV-1994.

XX

PF 21-APR-1994; 94WO-US004294.

XX

PR 23-APR-1993; 93US-00051741.

PR 29-OCT-1993; 93US-00143364.

XX

PA (EVAN/) EVANS H J.

PA (KINI/) KINI R M.

XX

PI Evans HJ, Kini RM;

XX

DR WPI; 1994-358186/44.

XX
PT Peptide homologue or analogue with constrained conformation - has proline
PT residues flanking the interaction site to impart greater, or more stable,
PT biological activity.
XX
PS Example 3; Page 38; 57pp; English.
XX
CC AAR67114-17 are anti-inflammatory peptides derived from naturally
CC occurring polypeptides that contain proline or proline/cysteine brackets.
CC These peptides are shortened to form fragments that contain one or more
CC interaction sites of interest. AAR67114-115 are deriv. from the
CC interleukin-8 receptor. The dose is 5-50 nanomoles. The peptides interact
CC with interleukin-8 and inhibit its ability to act as a chemo-attractant,
CC and thus inhibits the pro-inflammatory effects of the interleukin. The
CC data collected demonstrates that interaction sites possess activity when
CC present in a polypeptide that differs from the native form. Inclusion of
CC conformation-constraining moieties can have desirable effects on an
CC interaction site. (Also see AAR67011-113 and AAR67116-52 for analogues of
CC other biologically active peptides contg. an interaction site flanked by
CC conformation constraining gps., eg. RGD peptides.) (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 8 NKP 10

RESULT 49

AAR67036

ID AAR67036 standard; peptide; 11 AA.

XX

AC AAR67036;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1995 (first entry)

XX

DE Chemotactic peptide (CP-alphaPI1), contg. proline brackets.

XX

KW Chemotactic peptide; alpha-1 protease inhibitor; treatment;

KW enhance body defence mechanism; constrained conformation;

KW interaction site; mimic.

XX

OS Synthetic.

XX

PN WO9425482-A1.

XX

PD 10-NOV-1994.

XX

PF 21-APR-1994; 94WO-US004294.

XX

PR 23-APR-1993; 93US-00051741.

PR 29-OCT-1993; 93US-00143364.

XX

PA (EVAN/) EVANS H J.

PA (KINI/) KINI R M.

XX

PI Evans HJ, Kini RM;

XX

DR WPI; 1994-358186/44.

XX

PT Peptide homologue or analogue with constrained conformation - has proline
PT residues flanking the interaction site to impart greater, or more stable,
PT biological activity.

XX

PS Example 2; Page 24; 57pp; English.

XX

CC AAR67034-37 are chemotactic peptides derived from naturally occurring
CC polypeptides that contain proline or proline/cysteine brackets. These
CC peptides are shortened to form fragments that contain one or more
CC interaction sites of interest. AAR67036-7 originate from alpha-1 protease
CC inhibitor and attracts neutrophils and macrophages and hence will be
CC useful in enhancing body defence mechanisms at a required site. Dose is 5
CC -100 nanomoles. The data collected demonstrates that interaction sites
CC possess activity when present in a polypeptide that differs from the
CC native form. Inclusion of conformation-constraining moieties can have
CC desirable effects on an interaction site. (Also see AAR67011-33 and
CC AAR67038-152 for analogues of other biologically active peptides contg.
CC an interaction site flanked by conformation constraining gps., eg. RGD
CC peptides.) (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9

|||

Db 7 NKP 9

RESULT 50

AAR50563

ID AAR50563 standard; peptide; 11 AA.

XX

AC AAR50563;

XX

DT 25-MAR-2003 (revised)

DT 18-OCT-1994 (first entry)

XX

DE Amphiphillic peptide #112.

XX

KW Amphiphilic; ion forming; gynaecological malignancy; magainin; PGLa; XPF;

KW CPF; cecropin; sarcotoxin; melittin; apidaecin; defensin;

KW major basic protein; eosinophils; uterine; cervical; cancer;

KW bacterial permeability increasing protein; ovarian; stage IC.

XX

OS Synthetic.

XX
 PN WO9405313-A1.
 XX
 PD 17-MAR-1994.
 XX
 PF 16-AUG-1993; 93WO-US007798.
 XX
 PR 31-AUG-1992; 92US-00937462.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Jacob LS, Maloy WL, Baker MA;
 XX
 DR WPI; 1994-100851/12.
 XX
 PT Treating gynaecological tumours with amphiphilic peptide(s) - which form
 PT ion channels, e.g. magainin or PGLa peptide(s), partic. for treating
 PT ovarian, uterine or cervical cancers.
 XX
 PS Disclosure; Page 116; 130pp; English.
 XX
 CC The sequences given in AAR50452-568 represent amphiphilic, ion forming
 CC peptides which may be used to treat gynaecological malignancy. These
 CC peptides are based on magainin, PGLa, XPF or CPF, a cecropin, a
 CC sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of
 CC eosinophils or a bacterial permeability increasing protein. These
 CC peptides are esp. used to treat ovarian, esp. stage IC, uterine or
 CC cervical cancers. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 51

AAR55987

ID AAR55987 standard; peptide; 11 AA.

XX

AC AAR55987;

XX

DT 25-MAR-2003 (revised)

DT 19-DEC-1994 (first entry)

XX

DE Ion channel forming peptide.

XX

KW Ion channel forming peptide; tumour; skin disease; malignancy; melanoma;

KW carcinoma; basal cell; squamous cell; magainin; PGLa; CPF peptides;

KW cecropins; sarcotoxin; melittin; apidocin; defensins;

KW major basic protein; bacteria-permeability increasing protein; perforin.

XX

OS Synthetic.

XX
 PN WO9412206-A1.
 XX
 PD 09-JUN-1994.
 XX
 PF 03-DEC-1993; 93WO-US011885.
 XX
 PR 03-DEC-1992; 92US-00984957.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Jacob LS, Maloy WL;
 XX
 DR WPI; 1994-199965/24.
 XX
 PT Treating skin cancer with ion channel forming peptide(s) - e.g.
 PT magainins, mellitin etc., specifically for treating melanoma.
 XX
 PS Disclosure; Page 121; 136pp; English.
 XX
 CC The peptide is used to treat dermatological malignancies. It may be used
 CC to treat especially melanoma but also basal cell and squamous cell
 CC carcinomas. It can be used together with an ion which also
 CC inhibits/prevents growth of the target cell. Peptides used for such
 CC therapy include magainin, PGLa or CPF peptides; cercopins, sarcotoxins,
 CC mellitin, apidocins, defensins, major basic protein of eosinophils;
 CC bacteria-permeability increasing protein and perforin. See also AAQ55876-
 CC Q55997. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 52

AAR59065

ID AAR59065 standard; peptide; 11 AA.

XX

AC AAR59065;

XX

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX

DE Cancer treating, amphiphilic ion-channel forming peptide.

XX

KW Amphiphilic ion-channel forming peptide; cancer treatment;
 KW protease inhibitors.

XX

OS Synthetic.

XX

PN WO9419369-A1.

XX
 PD 01-SEP-1994.
 XX
 PF 22-FEB-1994; 94WO-US002121.
 XX
 PR 26-FEB-1993; 93US-00021607.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Herlyn M, Jacob LS, Maloy WL;
 XX
 DR WPI; 1994-294258/36.
 XX
 PT Treating cancerous growths - by administering biologically active
 PT peptide(s) and protease inhibitors.
 XX
 PS Claim 2; Page 106; 124pp; English.
 XX
 CC AAR59060 to AAR59066 are a group of amphiphilic ion-channel forming
 CC peptides conforming to the same generic sequence. Used in combination
 CC with one or more protease inhibitors and other amphiphilic ion-channel
 CC forming peptides or proteins; they are effective in the treatment of
 CC cancerous growths. In particular during surgery and radiation treatment
 CC they may be useful in inhibiting, preventing and/or destroying potential
 CC "loose" malignant cells capable of colonising other sites. (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 53

AAR71762

ID AAR71762 standard; peptide; 11 AA.

XX

AC AAR71762;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
 FT fluorescent label. See CC below. Also this amino acid can

FT be substituted by Lys or Orn."

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Beaudet A, Faure M, Gaudreau P;

XX

DR WPI; 1994-226757/28.

XX

PT New forescent markers for neurotensin receptors - useful for in vitro

PT labelling of neurotensin receptors on cell surface and to isolate

PT neurotensin-receptor expressing cells.

XX

PS Claim 2; Page 5; 19pp; English.

XX

CC The invention concerns highly sensitive fluorescent probes which allow

CC for rapid and precise characterisation of neurotensin receptor binding

CC properties on whole cells. The probes are of formula R1-C(=X)-R in which

CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue

CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin

CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-

CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in

CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via

CC the N-terminus in position 1. The N-terminal amino acid may also be

CC substd. by Lys or Orn. The present sequence represents one of the claimed

CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||
 Db 3 NKP 5

RESULT 54

AAR71761

ID AAR71761 standard; peptide; 11 AA.

XX

AC AAR71761;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Tyr or D-Tyr; and this residue is N-acylated with
FT fluorescent label. See CC below. Also this amino acid can
FT be substituted by Lys or Orn."
XX
PN EP606804-A2.
XX
PD 20-JUL-1994.
XX
PF 27-DEC-1993; 93EP-00403185.
XX
PR 30-DEC-1992; 92CA-02086453.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Beaudet A, Faure M, Gaudreau P;
XX
DR WPI; 1994-226757/28.
XX
PT New fluorescent markers for neurotensin receptors - useful for in vitro
PT labelling of neurotensin receptors on cell surface and to isolate
PT neurotensin-receptor expressing cells.
XX
PS Claim 2; Page 5; 19pp; English.
XX
CC The invention concerns highly sensitive fluorescent probes which allow
CC for rapid and precise characterisation of neurotensin receptor binding
CC properties on whole cells. The probes are of formula R1-C(=X)-R in which
CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue
CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin
CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-
CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in
CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via
CC the N-terminus in position 1. The N-terminal amino acid may also be
CC substd. by Lys or Orn. The present sequence represents one of the claimed
CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
| | |
Db 3 NKP 5

RESULT 55
AAR56948
ID AAR56948 standard; peptide; 11 AA.
XX
AC AAR56948;

XX
 DT 25-MAR-2003 (revised)
 DT 17-MAR-1995 (first entry)
 XX
 DE Peptide which neutralises bacterial endotoxin.
 XX
 KW septic shock; bacterial endotoxin; lipopolysaccharide; LPS;
 KW gram negative bacteria; conjugate moiety; septicemia; neutralising;
 KW longer activity; polyvinylpyrrolidone; dextran; hetastarch;
 KW polyvinyl alcohol; ion-channel forming; amphiphilic.
 XX
 OS Synthetic.
 XX
 PN W09413697-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 06-DEC-1993; 93WO-US011841.
 XX
 PR 07-DEC-1992; 92US-00987443.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Hendi M, Rao M, Williams TJ;
 XX
 DR WPI; 1994-217804/26.
 XX
 PT New conjugates of bioactive amphiphilic peptide(s) and conjugate moiety -
 PT are useful for treatment of septic shock.
 XX
 PS Disclosure; Page 115; 141pp; English.
 XX
 CC Septic shock is often due to the body's reaction to foreign
 CC lipopolysaccharide (LPS). The compounds of the invention neutralise
 CC bacterial endotoxins without neutralising essential proteins in the
 CC plasma of patients, eg.heparins. They also have longer duration of
 CC activity than unconjugated peptides. In general peptides such as this are
 CC ion-channel forming peptides.The compounds are biologically active
 CC peptides linked to a conjugate moiety, eg. carbohydrates, proteins,
 CC polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The
 CC conjugate moiety may be linked at the C- or N-terminal or internally of
 CC the peptide. AAR55591-631 and AAR56879-957 are examples of these peptide-
 CC conjugate moiety compounds (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 56
 AAR50448

ID AAR50448 standard; peptide; 11 AA.
 XX
 AC AAR50448;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-OCT-1994 (first entry)
 XX
 DE Amphiphilic peptide #113.
 XX
 KW Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
 KW antibiotic; antimicrobial; antifungal; antiparasitic; anticancer;
 KW antiviral; human; animal; plant; ion-channel; forming peptide.
 XX
 OS Synthetic.
 XX
 PN WO9405308-A1.
 XX
 PD 17-MAR-1994.
 XX
 PF 13-AUG-1993; 93WO-US007694.
 XX
 PR 28-AUG-1992; 92US-00936504.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Williams JI;
 XX
 DR WPI; 1994-100846/12.
 XX
 PT Purifying amphiphilic protein or peptide by solvent extn. - partic. for
 PT recombinant, ion-channel forming peptide(s) such as magainins, avoids use
 PT of chaotropic agents.
 XX
 PS Disclosure; Page 124; 135pp; English.
 XX
 CC The sequences given in AAR50336-451 are amphiphilic peptides which were
 CC isolated by the method of the invention. A material containing
 CC amphiphilic peptides such as these, was treated with a mixt. of aprotic
 CC organic solvent and alcohol to form a single miscible solution. This
 CC solution was then treated with a aqueous solution to form an aqueous
 CC phase solution containing the peptides and an organic solvent phase, and
 CC the peptides were isolated from the aqueous phase. The isolated peptides
 CC may be useful as antibiotic, antimicrobial, antifungal, antiparasitic,
 CC antitumour, anticancer, and/or antiviral agents for treatment of humans,
 CC animals or plants. These peptides are esp. ion-channel forming peptides
 CC which enable biologically active ions to enter cells. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 57

AAR82716

ID AAR82716 standard; peptide; 11 AA.

XX

AC AAR82716;

XX

DT 11-APR-1996 (first entry)

XX

DE Shrimp tropomyosin Asp N peptide (residues 258-269).

XX

KW Tropomyosin; allergen; IgE binding epitope; allergy; Pen i I; SA-II;
 KW crustacean; antiallergic; diagnosis; hypersensitivity.

XX

OS Artemia salina.

XX

PN US5449669-A.

XX

PD 12-SEP-1995.

XX

PF 10-NOV-1993; 93US-00149809.

XX

PR 10-NOV-1993; 93US-00149809.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Roa PVS, Metcalfe DD, Martin BM;

XX

DR WPI; 1995-327712/42.

XX

PT Antigenic and allergenic peptide(s) from shrimp tropomyosin and derivs. -
 PT used to diagnose and treat allergies to crustacea, esp. for
 PT desensitisation.

XX

PS Example 3; Col 7-8; 19pp; English.

XX

CC This Asp N peptide, a fragment of the shrimp major thermostable allergen
 CC of 34 kDa (tropomyosin), was generated in order to compare amino acid
 CC sequences of Pen i I with the deduced amino acid sequence of the alpha-
 CC chain of Drosophila melanogaster tropomyosin

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5

|||

Db 6 KEK 8

RESULT 58

AAW21220

ID AAW21220 standard; peptide; 11 AA.

XX

AC AAW21220;
 XX
 DT 29-JUL-1997 (first entry)
 XX
 DE Farnesyl synthetase derived signal oligopeptide #20.
 XX
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
 XX
 OS Homo sapiens.
 XX
 PN WO9519568-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 12-JAN-1995; 95WO-US000575.
 XX
 PR 14-JAN-1994; 94US-00182248.
 XX
 PA (RATH/) RATH M.
 XX
 PI Rath M;
 XX
 DR WPI; 1995-263953/34.
 XX
 PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication between
 PT protein(s).
 XX
 PS Claim 5; Page 26; 88pp; English.
 XX
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface of the
 CC protein and are represented by the hydrophilicity maxima of the protein.
 CC These peptides are enriched in charged amino acids arranged with neutral
 CC spacer amino acids. The specific signal character of these oligopeptides
 CC is determined by a characteristic combination of conformation and charge
 CC within the signal sequence. These oligopeptides may be used as vaccines
 CC in the treatment of human disease, as competitive inhibitors to prevent
 CC or reduce the metabolic action or interaction of a selected protein by
 CC blocking its specific signal sequences, or as therapeutic agents to
 CC function as feedback regulators to reduce synthesis rate of a selected
 CC protein. These peptides may be modified by omitting one or more amino
 CC acids at the N- and/or C-terminal, by substituting one or more amino
 CC acids without consideration of charge and polarity, by substituting one
 CC or more amino acids with amino acid residues with similar charge and/or
 CC polarity, by omitting one or more amino acids or a combination of these
 XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 59

AAR76917

ID AAR76917 standard; peptide; 11 AA.

XX

AC AAR76917;

XX

DT 08-MAR-1996 (first entry)

XX

DE Thymosin alpha-1 peptide analogue #23.

XX

KW Thymosin alpha-1; analogue; immune system modulator; alpha-interferon;
KW gamma-interferon; macrophage migration inhibitory factor; T-cell marker;
KW interleukin-2 receptor; helper T-cell; solid phase synthesis;
KW immunodeficiency; therapy; AIDS; HIV; immunodepravation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "optionally amidated Pro or amidated Gly"

XX

PN WO9520602-A2.

XX

PD 03-AUG-1995.

XX

PF 18-JAN-1995; 95WO-US000617.

XX

PR 28-JAN-1994; 94US-00188232.

XX

PA (ALPH-) ALPHA 1 BIOMEDICALS INC.

XX

PI Wang S;

XX

DR WPI; 1995-275412/36.

XX

PT New thymosin alpha-1 peptide analogues - for the treatment of
PT immunodeficiency diseases and the reconstitution of immune functions in
PT immuno-depressed patients.

XX

PS Claim 7; Page ?; 24pp; English.

XX

CC The sequences represented by AAR76895-R76935 are thymosin alpha-1
CC analogues. Thymosin alpha-1 is an immune system modulator. Thymosin alpha
CC -1 activity includes, stimulation of alpha- and gamma-interferon
CC production, increasing macrophage migration inhibitory factor production,
CC inducing expression of T-cell markers (including interleukin-2

CC receptors), and improving helper T-cell activity. These sequences
CC function like natural thymosin alpha-1, and are easy to produce. These
CC sequences were synthesised by solid phase synthesis on a 4-
CC methylbenzhydrylamine resin. The peptides were cleaved from this resin
CC using trifluoromethane sulfonic acid (TFS). These sequences can be used
CC to reconstitute immune functions in immunodeprived and immunodepressed
CC patients. They can also be used in the treatment of immunodeficiency
CC diseases

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 1 KKE 3

RESULT 60

AAR78790

ID AAR78790 standard; peptide; 11 AA.

XX

AC AAR78790;

XX

DT 25-MAR-2003 (revised)

DT 23-NOV-1995 (first entry)

XX

DE Rac1 (127-137) peptide sequence.

XX

KW superoxide inhibition; phagocyte; GTP-binding; G protein; Rac;

KW mastoparan; antiinflammatory; inflammation; ICS4; GAP.

XX

OS Synthetic.

XX

PN WO9503819-A1.

XX

PD 09-FEB-1995.

XX

PF 29-JUL-1994; 94WO-US008631.

XX

PR 02-AUG-1993; 93US-00102944.

PR 15-NOV-1993; 93US-00156552.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Bokoch GM, Curnutte JT;

XX

DR WPI; 1995-082027/11.

XX

PT New peptide(s) inhibiting super:oxide prodn. in phagocyte(s) - derived

PT e.g. from GTP binding proteins or mastoparan, useful for inhibiting

PT inflammation, e.g. in cases of auto:immune disease, gout, asthma, etc.

XX

PS Claim 5; Page 93; 107pp; English.

XX

CC An optionally substituted, non-toxic peptide of not more than 40 amino
CC acids in length is claimed, the peptide being capable of inhibiting
CC superoxide prodn. in phagocytic cells and therefore being useful in
CC inhibiting inflammation and treating inflammatory disorders such as
CC autoimmune diseases, gout, ARDS, asthma, myocardial infarction and
CC various dermatological disorders. Preferably the protein is a low mol.
CC wt. GTP binding protein (LMWG), a mastoparan, or an ICS4 peptide. The
CC present sequence is a specifically claimed example of a preferred
CC peptide. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5

|||

Db 4 KEK 6

RESULT 61

AAR86397

ID AAR86397 standard; peptide; 11 AA.

XX

AC AAR86397;

XX

DT 19-APR-1996 (first entry)

XX

DE Soybean-derived phagocytosis-promoting immunostimulatory peptide 3.

XX

KW Immunostimulatory peptide; phagocytosis; active oxygen; soybean.

XX

OS Soybean.

XX

PN JP07224093-A.

XX

PD 22-AUG-1995.

XX

PF 11-FEB-1994; 94JP-00037707.

XX

PR 11-FEB-1994; 94JP-00037707.

XX

PA (HOHN) HOHNEN CORP.

XX

DR WPI; 1995-331084/43.

XX

PT Novel peptide(s) and immuno:stimulatory compsn. contg. them - promote

PT phagocytosis and active oxygen prodn.

XX

PS Claim 1; Page 2; 8pp; Japanese.

XX

CC Peptides AAR86395-R86404 are novel immunostimulatory peptides that
CC promote phagocytosis as well as the prodn. of active oxygen. The peptides
CC were isolated from soybeans by conventional chromatography, or were
CC synthesised by Fmoc chemistry

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 9 NKP 11

RESULT 62

AAR90259

ID AAR90259 standard; peptide; 11 AA.

XX

AC AAR90259;

XX

DT 10-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #111 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono- or di-substd. by
FT lipophilic moiety, esp. octanoyl"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U, Williams TJ, Mclane M;

XX

DR WPI; 1995-263826/34.

XX

PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
PT antitumour agents.

XX

PS Claim 25; Page 108; 139pp; English.

XX

CC The present peptide is a specific example corresp. to a highly generic
CC formula for ion channel forming peptides (ionophores). These ionophores
CC are known to have a broad range of potent antibiotic activity against
CC microorganisms including gram-positive and gram-negative bacteria, fungi,

CC viruses, protozoa and parasites. N-terminal modification (pref. mono-
CC substn. by octanoyl) to produce an ion-channel forming peptide having a
CC lipophilic N-terminus increases the biological activity of the peptides
CC against target cells, viruses and virally-infected cells, compared to
CC peptides substd. with an acetyl group at the N-terminus. Compositions
CC comprising the peptides with lipophilic modifications are claimed for
CC inhibiting growth of a target cell, virus or virally-infected cell

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 63

AAR91788

ID AAR91788 standard; peptide; 11 AA.

XX

AC AAR91788;

XX

DT 11-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #123 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;

KW magainin; inhibition; cell growth; viral replication; ionophore;

KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;

KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono-substd. by
FT octanoyl"

FT Modified-site 11

FT /note= "C-terminal amide"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U, Williams TJ, Mclane M;

XX

DR WPI; 1995-263826/34.

XX

PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
PT antitumour agents.
XX
PS Example 1; Page 111; 139pp; English.
XX
CC Various ion channel forming peptides (ionophores) in C-terminal amide
CC form were modified by N-terminal substn. with a lipophilic group and then
CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
CC that when a biologically active peptide is substd. with a lipophilic
CC moiety, the peptide has increased activity against a range of
CC microorganisms. Compositions comprising such peptides with lipophilic
CC modifications are claimed for inhibiting growth of a target cell, virus
CC or virally-infected cell. Minimum inhibitory concentrations (in
CC microgram/ml) for the present peptide against S, P, E and C,
CC respectively, were: 32, 16, 32 and 32
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 64
AAR91787

ID AAR91787 standard; peptide; 11 AA.
XX
AC AAR91787;
XX
DT 11-JUL-1996 (first entry)
XX
DE Ion-channel forming peptide #122 with lipophilic N-terminal group.
XX
KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal amino group is mono-substd. by
FT octanoyl"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN W09519370-A1.
XX
PD 20-JUL-1995.
XX

PF 18-JAN-1995; 95WO-US000714.
 XX
 PR 18-JAN-1994; 94US-00184462.
 XX
 PA (MAGA-) MAGAININ PHARM INC.
 XX
 PI Kari U, Williams TJ, McLane M;
 XX
 DR WPI; 1995-263826/34.
 XX
 PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
 PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
 PT antitumour agents.
 XX
 PS Example 1; Page 111; 139pp; English.
 XX
 CC Various ion channel forming peptides (ionophores) in C-terminal amide
 CC form were modified by N-terminal substn. with a lipophilic group and then
 CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
 CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
 CC that when a biologically active peptide is substd. with a lipophilic
 CC moiety, the peptide has increased activity against a range of
 CC microorganisms. Compositions comprising such peptides with lipophilic
 CC modifications are claimed for inhibiting growth of a target cell, virus
 CC or virally-infected cell. Minimum inhibitory concentrations (in
 CC microgram/ml) for the present peptide against S, P, E and C,
 CC respectively, were: 32, 32, 64 and 64
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 7 AKK 9

RESULT 65

AAR92106

ID AAR92106 standard; peptide; 11 AA.

XX

AC AAR92106;

XX

DT 19-MAY-1996 (first entry)

XX

DE Human RIZ cr2 fragment.

XX

KW Retinoblastoma protein-interacting zinc finger; RIZ; cell proliferation;
 KW tumour; cancer; neuroblastoma; melanoma; diagnosis; therapy;
 KW transcription.

XX

OS Homo sapiens.

XX

PN WO9606168-A2.

XX

PD 29-FEB-1996.
 XX
 PF 18-AUG-1995; 95WO-US010574.
 XX
 PR 18-AUG-1994; 94US-00292683.
 PR 06-MAR-1995; 95US-00399411.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Huang S;
 XX
 DR WPI; 1996-151371/15.
 XX
 PT Nucleic acid encoding mammalian retinoblastoma protein-interacting zinc
 PT finger - used to identify cell proliferation modulating agents for
 PT treatment of tumours, esp. neuroblastoma and melanoma, also used for
 PT cancer diagnosis.
 XX
 PS Claim 19; Page 102; 142pp; English.
 XX
 CC Active fragments of mammalian retinoblastoma protein-interacting zinc
 CC finger (RIZ), such as rat RIZ cr2 fragment (AAR92105) and human RIZ cr2
 CC fragment (AAR92106), bind to retinoblastoma, interact with transcription
 CC factors and can be involved in regulating transcription. They are
 CC produced by recombinant DNA methods, by peptide synthesis or by enzymatic
 CC cleavage of RIZ. RIZ or its active fragments (see also AAR92107-09) can
 CC be obtd. by recombinant DNA methods, and used to identify agents that
 CC modulate cell proliferation and thereby treat tumour growth or
 CC neurodegenerative disorders
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
 |||
 Db 6 EKP 8

RESULT 66

AAR92105

ID AAR92105 standard; peptide; 11 AA.

XX

AC AAR92105;

XX

DT 19-MAY-1996 (first entry)

XX

DE Rat RIZ cr2 fragment.

XX

KW Retinoblastoma protein-interacting zinc finger; RIZ; cell proliferation;
 KW tumour; cancer; neuroblastoma; melanoma; diagnosis; therapy;
 KW transcription.

XX

OS Rattus sp.

XX

PN WO9606168-A2.
 XX
 PD 29-FEB-1996.
 XX
 PF 18-AUG-1995; 95WO-US010574.
 XX
 PR 18-AUG-1994; 94US-00292683.
 PR 06-MAR-1995; 95US-00399411.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Huang S;
 XX
 DR WPI; 1996-151371/15.
 XX
 PT Nucleic acid encoding mammalian retinoblastoma protein-interacting zinc
 PT finger - used to identify cell proliferation modulating agents for
 PT treatment of tumours, esp. neuroblastoma and melanoma, also used for
 PT cancer diagnosis.
 XX
 PS Claim 18; Page 102; 142pp; English.
 XX
 CC Active fragments of mammalian retinoblastoma protein-interacting zinc
 CC finger (RIZ), such as rat RIZ cr2 fragment (AAR92105) and human RIZ cr2
 CC fragment (AAR92106), bind to retinoblastoma, interact with transcription
 CC factors and can be involved in regulating transcription. They are
 CC produced by recombinant DNA methods, by peptide synthesis or by enzymatic
 CC cleavage of RIZ. RIZ or its active fragments (see also AAR92107-09) can
 CC be obtd. by recombinant DNA methods, and used to identify agents that
 CC modulate cell proliferation and thereby treat tumour growth or
 CC neurodegenerative disorders
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
 |||
 Db 6 EKP 8

RESULT 67
 AAR85318
 ID AAR85318 standard; peptide; 11 AA.
 XX
 AC AAR85318;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-AUG-1996 (first entry)
 XX
 DE Human retinoic acid receptor RAR-beta (human liver HAP) peptide-2.
 XX
 KW HAP; liver; hepatoma; retinoic acid receptor; RAR-beta; psoriasis;
 KW atherosclerosis; rheumatoid arthritis.
 XX

OS Homo sapiens.
 XX
 PN US5468617-A.
 XX
 PD 21-NOV-1995.
 XX
 PF 02-FEB-1994; 94US-00190555.
 XX
 PR 16-DEC-1987; 87US-00133687.
 PR 17-DEC-1987; 87US-00134130.
 PR 20-JUN-1988; 88US-00209009.
 PR 30-NOV-1988; 88US-00278136.
 PR 30-MAR-1989; 89US-00330405.
 PR 21-AUG-1991; 91US-00751612.
 PR 30-MAR-1992; 92US-00860577.
 PR 11-DEC-1992; 92US-00989902.
 PR 22-JUL-1993; 93US-00095706.
 XX
 PA (TIOL/) TIOLLAIS P.
 PA (DEJE/) DEJEAN A.
 PA (KRUS/) KRUST A.
 PA (PETK/) PETKOVICH M.
 PA (DTHE/) BLAUDIN DE THE H.
 PA (MARC/) MARCHIO A.
 PA (BRAN/) BRAND N.
 PA (CHAM/) CHAMBON P.
 XX
 PI Brand N, Chambon P, Blaudin De The H, Marchio A, Dejean A;
 PI Petkovich M, Krust A, Tiollais P;
 XX
 DR WPI; 1996-010094/01.
 XX
 PT Method for screening for retinoic acid receptor-beta (ant)agonists -
 PT useful for blood testing and for treatment of rheumatoid arthritis,
 PT psoriasis, atherosclerosis etc.
 XX
 PS Claim 7; Col 39-40; 35pp; English.
 XX
 CC This RAR-beta peptide-2 fragment is part of a protein which may be
 CC expressed recombinantly in bacterial host cells such as Escherichia coli
 CC TG-1. The protein, which is free from human, blood-derived protein, forms
 CC a complex with an agonist or antagonist. The protein may be used in a
 CC novel method for assaying a fluid for the presence of an agonist or
 CC antagonist to retinoic acid receptor, RAR-beta. (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 2 KKE 4
 |||
 Db 7 KKE 9

RESULT 68

AAW18499

ID AAW18499 standard; peptide; 11 AA.

XX

AC AAW18499;

XX

DT 19-FEB-1998 (first entry)

XX

DE Amino-terminal peptide 1 associated with novel helicase.

XX

KW Nucleic acid binding protein; helicase; leflunomide; assaying;
 KW 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole; identification;
 KW anticancer; antiatherosclerotic; immunosuppressant; sequencing;
 KW antiinflammatory; antiviral; antifungal; antibacterial; treatment;
 KW Alzheimer's disease; cancer; rheumatism; arthrosis; determination;
 KW atherosclerosis; osteoporosis; acute infection; chronic infection;
 KW autoimmune disease; diabetes; organ transplant; isolation;
 KW amino-terminal.

XX

OS Homo sapiens.

XX

PN DE19545126-A1.

XX

PD 05-JUN-1997.

XX

PF 04-DEC-1995; 95DE-01045126.

XX

PR 04-DEC-1995; 95DE-01045126.

XX

PA (FARH) HOECHST AG.

XX

PI Kirschbaum B, Muellner S, Bartlett R;

XX

DR WPI; 1997-299388/28.

XX

PT New nucleic acid binding protein with helicase activity - is strongly
 PT induced by leflunomide, used to isolate specific binding RNA and for
 PT identifying substances with anticancer, antiviral etc. activities.

XX

PS Example 4; Page 15; 28pp; German.

XX

CC The present sequence is an amino-terminal peptide associated with a novel
 CC nucleic acid binding protein with helicase activity, the mRNA of which
 CC (or its translation products) is strongly expressed in presence of
 CC leflunomide, i.e. 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole, or a
 CC compound with similar activity. The helicase can be used in assay systems
 CC to identify/discover anticancer, antiatherosclerotic, immunosuppressing,
 CC antiinflammatory, antiviral, antifungal and antibacterial agents, e.g. to
 CC treat Alzheimer's disease, cancer, rheumatism, arthrosis,
 CC atherosclerosis, osteoporosis, acute/chronic infections, autoimmune
 CC disease, diabetes and complications of organ transplants, and to isolate
 CC or determine the sequences of specific binding RNA

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
 | | |
Db 9 KKE 11

RESULT 69

AAW24438

ID AAW24438 standard; peptide; 11 AA.

XX

AC AAW24438;

XX

DT 30-SEP-1997 (first entry)

XX

DE Nucleic acid (NA) binding peptide used in NA delivery to cells.

XX

KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;

KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.

XX

OS Synthetic.

XX

PN WO9640958-A1.

XX

PD 19-DEC-1996.

XX

PF 23-APR-1996; 96WO-US005679.

XX

PR 07-JUN-1995; 95US-00484777.

XX

PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX

PI Smith LC, Sparrow JT, Woo SL;

XX

DR WPI; 1997-052345/05.

XX

PT Nucleic acid transporter useful in gene therapy - contains binding
PT complex associated with surface and nuclear ligands and lysis agent.

XX

PS Disclosure; Page 49; 125pp; English.

XX

CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
CC condensing and stabilising a NA. The peptides can be conjugated to a
CC lytic peptide to form a nucleic acid transporter system. The lysis agent
CC forms an alpha-helical structure. The transporter system is used to
CC deliver nucleic acid to a cell and for treating humans by gene therapy.
CC By taking advantage of the characteristics of both the lysis agents and
CC the binding molecules, delivery of the nucleic acid is enhanced. Specific
CC lysis agents are capable of releasing the nucleic acid into the cellular
CC interior from the endosome. Release is efficient without
CC endosomal/lysosomal degradation. Once released the binding complexes help
CC target the nucleic acid to the nucleus

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 70

AAW35836

ID AAW35836 standard; peptide; 11 AA.

XX

AC AAW35836;

XX

DT 27-FEB-1998 (first entry)

XX

DE Soymetide 3 a soybean protein-derived peptide.

XX

KW Soymetide; soybean; antialopecia agent; alopecia; carcinostatic;
KW prevention; amelioration.

XX

OS Glycine max.

XX

PN JP09249535-A.

XX

PD 22-SEP-1997.

XX

PF 13-MAR-1996; 96JP-00084667.

XX

PR 13-MAR-1996; 96JP-00084667.

XX

PA (HOHN) HOHNEN CORP.

XX

DR WPI; 1997-529971/49.

XX

PT Anti-alopecia agent containing soybean protein-derived peptide -
PT especially effective against alopecia induced by carcinostatic agents.

XX

PS Claim 1; Page 2; 6pp; Japanese.

XX

CC An anti-alopecia agent has been developed which comprises one or more
CC soybean protein-derived peptides (designated Soymetides). The present
CC sequence represents a specifically claimed soymetide. This agent is
CC especially useful for the prevention and amelioration of alopecia caused
CC by administration of carcinostatic agents. Soymetide has low toxicity

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 9 NKP 11

RESULT 71

AAW09909
 ID AAW09909 standard; peptide; 11 AA.
 XX
 AC AAW09909;
 XX
 DT 16-OCT-1997 (first entry)
 XX
 DE Prostate specific membrane antigen peptide PSM-P26.
 XX
 KW Prostate specific membrane antigen; PSMA; prostate specific antigen; PSA;
 KW prostate cancer; adoptive cellular immunotherapy; therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO9704802-A1.
 XX
 PD 13-FEB-1997.
 XX
 PF 29-JUL-1996; 96WO-US012389.
 XX
 PR 31-JUL-1995; 95US-00509254.
 XX
 PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.
 XX
 PI Murphy GP, Boynton AL, Tjoa BA;
 XX
 DR WPI; 1997-145375/13.
 XX
 PT Use of dendritic cells for prostate cancer immuno:therapy - the cells are
 PT exposed to prostate cancer antigen, then administered to the patient
 PT where they activate and proliferate T-cells.
 XX
 PS Claim 3; Page 47; 69pp; English.
 XX
 CC Peptide PSM-P26 (AAW09909) corresponds to amino acid residues 398-408 of
 CC prostate specific membrane antigen (PSMA). A method for producing a
 CC cancer growth inhibiting response comprises exposing human dendritic
 CC cells (DCs) to PSM-P26 or other PSMA or prostate specific antigen
 CC peptides (see also AAW09889-908 and AAW09910-26), and then administering
 CC the DCs to a prostate cancer patient to activate T cell responses in
 CC vivo. Alternatively, the T cell response is activated in vitro and the T
 CC cells are then administered to the patient. In either case, the DCs are
 CC used to elicit an immunotherapeutic growth inhibiting response against a
 CC primary or metastatic prostate tumour. PSM-P26 was selected to be
 CC presented by DCs to activate T cells of a patient which match the A11
 CC haplotype
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
 |||
 Db 9 KKE 11

RESULT 72

AAW04613

ID AAW04613 standard; peptide; 11 AA.

XX

AC AAW04613;

XX

DT 13-AUG-1997 (first entry)

XX

DE Physalaemin peptide for mass spectrometry analysis.

XX

KW Mass spectrometry; polymer analysis; biopolymer analysis.

XX

OS Synthetic.

XX

PN W09636986-A1.

XX

PD 21-NOV-1996.

XX

PF 17-MAY-1996; 96WO-US007146.

XX

PR 19-MAY-1995; 95US-00446055.

PR 19-MAY-1995; 95US-00447175.

XX

PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.

XX

PI Patterson DH, Tarr GE;

XX

DR WPI; 1997-012308/01.

XX

PT Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins, etc.

PT - by obtaining mass to charge ratios of polymer fragments, pref. using

PT mass spectrometer, and performing statistical analysis.

XX

PS Example 2; Page 32; 86pp; English.

XX

CC A method of obtaining sequence information about a polymer (e.g. DNA, RNA, peptide nucleic acids, proteins, peptides and carbohydrates)

CC comprising monomers of known mass has been claimed. The present sequence represents a physalaemin peptide, and was used as an example as a

CC digestion before analysis by mass spectrometry, using this novel on-plate strategy. Total sequence information from a nine well digestion can be

CC represented in a single digestion or it is often derived from two or more wells. The methods, apparatus and kit (claimed) can be used for the

CC analysis of polymers, particularly biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides and carbohydrates. It provides a rapid,

CC automated and cost effective sequencing of polymers, with a statistical certainty

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8

|||

RESULT 73

AAW35540

ID AAW35540 standard; peptide; 11 AA.

XX

AC AAW35540;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

XX

DE Biotin-labelled model peptide SEQ ID NO:80 from WO9738011.

XX

KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;

KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Labelled with biotin"

XX

PN WO9738011-A1.

XX

PD 16-OCT-1997.

XX

PF 03-APR-1997; 97WO-DK000146.

XX

PR 03-APR-1996; 96DK-00000398.

XX

PA (PEPR-) PEPRESEARCH AS.

XX

PI Heegaard PMH, Jakobsen PH;

XX

DR WPI; 1997-512645/47.

XX

PT Non-dendritic peptide carrier linked to a solid phase - useful as a

PT diagnostic agent and as a scaffold for production of chemical

PT derivatives.

XX

PS Example 28; Page 153; 262pp; English.

XX

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.

CC Where (A) comprises 10-50 amino acids capable of forming a secondary

CC structure in a benign buffer after liberation from the solid phase, and

CC further the (A)-solid phase complex comprises an immunogenic substance

CC and/or an immune mediator coupled on (A). The present sequence represents

CC a peptide used in an example from the present invention. An (A)-solid

CC phase complex can be used as a scaffold for the production of chemical

CC derivatives, characterised by covalently attaching molecules at

CC attachment points. Alternatively (A) is used as a scaffold-peptide for

CC the incorporation into an Immunostimulating Complex (Iscom) resulting an

CC (A)-Iscom complex which is used for the chemical coupling of antigenic

CC substances in an aqueous solution by conjugation. (A) derivatised with

CC one or more peptides having fibronectin-, laminin- or vitronectin-like

CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules
CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
CC correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9

|||

Db 7 NKP 9

RESULT 74

AAW35543

ID AAW35543 standard; peptide; 11 AA.

XX

AC AAW35543;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

XX

DE Immunization DNDPC SEQ ID NO:87 from WO9738011.

XX

KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX

OS Synthetic.

XX

PN WO9738011-A1.

XX

PD 16-OCT-1997.

XX

PF 03-APR-1997; 97WO-DK000146.

XX

PR 03-APR-1996; 96DK-00000398.

XX

PA (PEPR-) PEPRESEARCH AS.

XX

PI Heegaard PMH, Jakobsen PH;

XX

DR WPI; 1997-512645/47.

XX

PT Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives.

XX

PS Example 31; Page 156; 262pp; English.

XX

CC A non-dendritic peptide carrier (A) has been developed which is coupled

CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence represents
 CC a peptide used in an example from the present invention. An (A)-solid
 CC phase complex can be used as a scaffold for the production of chemical
 CC derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an Immunostimulating Complex (Iscom) resulting an
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||
 Db 4 NKP 6

RESULT 75

AAW83278

ID AAW83278 standard; peptide; 11 AA.

XX

AC AAW83278;

XX

DT 08-FEB-1999 (first entry)

XX

DE NPF motif EH domain binding peptide #59.

XX

KW Human; cytoplasmic protein; EH-containing protein; eps15; eps15R;
 KW eps15 homology; intracellular interaction; EH domain binding specificity;
 KW signal transducer; NPF motif; h-NUMB; h-NUMB-R; h-RAB; h-RAB-R; ehb3;
 KW ehb10; ehb21; cell proliferation; diagnosis; detection.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9846744-A1.

XX

PD 22-OCT-1998.

XX

PF 06-APR-1998; 98WO-IT000077.

XX

PR 15-APR-1997; 97IT-MI000868.

XX

PA (EUON-) IST EURO DI ONCOLOGIA SRL.

XX

PI Salcini AE, Doria M, Pelicci PG, Di Fiore PP;

XX

DR WPI; 1998-594574/50.

XX

PT New isolated EH domain binding proteins and peptide(s) - obtained using
PT signal transducers eps15 and eps15R containing EH domains by detecting
PT specific binding activity.

XX

PS Claim 11; Page 72; 90pp; English.

XX

CC The present invention describes a new intracellular interactor and novel
CC protein:protein interaction (EH) domain binding protein having (parts of)
CC one of the following human derived sequences designated: (I) h-NUMB; (II)
CC h-NUMB-R; (III) h-RAB-R; (IV) ehb3; (V) ehb10; or (VI) ehb21. The present
CC invention also describes peptides containing at least one NPF (Asp-Pro-
CC Phe) motif, able to bind to a protein with at least one EH domain. The
CC proteins with a NPF-containing peptide or the peptides themselves can be
CC used to identify and purify EH containing proteins. Antisense RNA,
CC complementary to mRNA encoding h-NUMB, h-NUMB-R, h-RAB-R, ehb3, ehb10, or
CC ehb21, can be used for diagnostic and therapeutic uses. Products from the
CC present invention can also be used to develop agents for use in control
CC of cell proliferation. AAW83220 to AAW83284 represent NPF motif EH domain
CC binding peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKP 6

|||

Db 1 EKP 3

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Job time : 45.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
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Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

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Minimum DB seq length: 11
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3	27.3	11	1	US-07-657-769B-7	Sequence 7, Appli	
4	3	27.3	11	1	US-07-657-769B-47	Sequence 47, Appl	
5	3	27.3	11	1	US-08-087-423-11	Sequence 11, Appl	
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8	3	27.3	11	1	US-08-116-733-31	Sequence 31, Appl	
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15	3	27.3	11	1	US-08-116-733-41	Sequence 41, Appl
16	3	27.3	11	1	US-08-167-035-38	Sequence 38, Appl
17	3	27.3	11	1	US-08-428-488-16	Sequence 16, Appl
18	3	27.3	11	1	US-08-434-120-112	Sequence 112, App
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35	3	27.3	11	1	US-08-475-263-37	Sequence 37, Appl
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44	3	27.3	11	1	US-08-485-886-28	Sequence 28, Appl
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49	3	27.3	11	1	US-08-485-886-181	Sequence 181, App
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56	3	27.3	11	2	US-08-477-362-28	Sequence 28, Appl
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58	3	27.3	11	2	US-08-477-362-39	Sequence 39, Appl
59	3	27.3	11	2	US-08-477-362-52	Sequence 52, Appl
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61	3	27.3	11	2	US-08-477-362-181	Sequence 181, App
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79	3	27.3	11	2	US-09-207-621-29	Sequence 29, Appl
80	3	27.3	11	2	US-09-207-621-108	Sequence 108, App
81	3	27.3	11	2	US-08-532-818-29	Sequence 29, Appl
82	3	27.3	11	2	US-08-532-818-108	Sequence 108, App
83	3	27.3	11	2	US-08-343-443B-70	Sequence 70, Appl
84	3	27.3	11	2	US-08-343-443B-72	Sequence 72, Appl
85	3	27.3	11	2	US-08-343-443B-86	Sequence 86, Appl
86	3	27.3	11	3	US-08-473-489A-20	Sequence 20, Appl
87	3	27.3	11	3	US-08-473-489A-28	Sequence 28, Appl
88	3	27.3	11	3	US-08-473-489A-37	Sequence 37, Appl
89	3	27.3	11	3	US-08-473-489A-39	Sequence 39, Appl
90	3	27.3	11	3	US-08-473-489A-52	Sequence 52, Appl
91	3	27.3	11	3	US-08-473-489A-54	Sequence 54, Appl
92	3	27.3	11	3	US-08-473-489A-181	Sequence 181, App
93	3	27.3	11	3	US-08-159-339A-1146	Sequence 1146, Ap
94	3	27.3	11	3	US-08-516-859A-6	Sequence 6, Appli
95	3	27.3	11	3	US-08-516-859A-91	Sequence 91, Appl
96	3	27.3	11	3	US-09-231-797-29	Sequence 29, Appl
97	3	27.3	11	3	US-09-231-797-108	Sequence 108, App
98	3	27.3	11	3	US-08-934-224-29	Sequence 29, Appl
99	3	27.3	11	3	US-08-934-224-108	Sequence 108, App
100	3	27.3	11	3	US-09-188-579-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-08-111-939-7

; Sequence 7, Application US/08111939

; Patent No. 5460951

; GENERAL INFORMATION:

; APPLICANT: Kawai, Shinji

; APPLICANT: Takeshita, Sunao

; APPLICANT: Okazaki, Makoto

; APPLICANT: Amann, Egon

; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like

; TITLE OF INVENTION: Protein and Process for its Production

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,939
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324033/92
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 230029/92
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 02481.1321-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: OSF 5.1 (antigen peptide)
; DESCRIPTION: segment of mouse OSF-5 from the 116th to
; DESCRIPTION: the 126th amino acid residue
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-111-939-7

```

```

Query Match          36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KEKP 6
        ||||
Db      3 KEKP 6

```

```

RESULT 2
US-09-100-930A-10
; Sequence 10, Application US/09100930A
; Patent No. 6248549
; GENERAL INFORMATION:
; APPLICANT: Van Eyk, Jennifer E.
; APPLICANT: Mak, Alan S.
; APPLICANT: Cote, Graham P.
; TITLE OF INVENTION: Methods of Modulating Muscle Contraction
; FILE REFERENCE: 1997-021-03US
; CURRENT APPLICATION NUMBER: US/09/100,930A
; CURRENT FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/050,478

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; PRIOR FILING DATE: 1997-06-23
 ; PRIOR APPLICATION NUMBER: 60/089,505
 ; PRIOR FILING DATE: 1998-06-16
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(11)
 ; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (11)
 ; OTHER INFORMATION: Targeted Ser phospho-amino acid
 US-09-100-930A-10

Query Match 36.4%; Score 4; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKE 4
 ||||
 Db 7 AKKE 10

RESULT 3

US-07-657-769B-7

; Sequence 7, Application US/07657769B
 ; Patent No. 5256766
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
 ; TITLE OF INVENTION: PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IRELL & MANELLA
 ; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
 ; CITY: MENLO PARK
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/657,769B
 ; FILING DATE: 19910219
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2000-0502.00
 ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-657-769B-7

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 4

US-07-657-769B-47

; Sequence 47, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-657-769B-47

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 5

US-08-087-423-11

; Sequence 11, Application US/08087423
; Patent No. 5455228

; GENERAL INFORMATION:

; APPLICANT: Coller, Barry S.
; APPLICANT: Prestwich, Glenn D.
; TITLE OF INVENTION: Peptidase Resistant Thrombin
; TITLE OF INVENTION: Receptor Thrombin Ligand
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11753

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 5.25 inch, 360 KbL
; COMPUTER: IBM XT Compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/087,423
; FILING DATE: 02-July-1993
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA: No. 5455228e

; ATTORNEY/AGENT INFORMATION:

; NAME: MORRIS, ARLENE D.
; REGISTRATION NUMBER: 32,657
; REFERENCE/DOCKET NUMBER: 178-150

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 Amino Acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

; FEATURE:

; NAME/KEY: Modified-Site
; LOCATION: 1

; OTHER INFORMATION: /No. 5455228e = "D-Ser"

US-08-087-423-11

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 6

US-08-193-521-18

; Sequence 18, Application US/08193521

; Patent No. 5470950

; GENERAL INFORMATION:

; APPLICANT: Maloy, W. Lee

; APPLICANT: Kari, U. Prasad

; APPLICANT: Williams, Jon I.

; TITLE OF INVENTION: Biologically Active Peptide

; TITLE OF INVENTION: Compositions and Uses Therefor

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi & Stewart

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: DW4.V2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/193,521

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/870,960

; FILING DATE:

; APPLICATION NUMBER: 07/760,054

; FILING DATE: 13-SEP-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Olstein, Elliot M.

; REGISTRATION NUMBER: 24,025

; REFERENCE/DOCKET NUMBER: 421250-161

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide,
; OTHER INFORMATION: and/or may be acetylated at
; OTHER INFORMATION: N-terminus.
US-08-193-521-18

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 7

US-08-116-733-1
; Sequence 1, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-1

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 8

US-08-116-733-31

; Sequence 31, Application US/08116733

; Patent No. 5516632

; GENERAL INFORMATION:

; APPLICANT: PALKER, Thomas J.

; APPLICANT: HAYNES, Barton F.

; TITLE OF INVENTION: SYNTHETIC PEPTIDES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/116,733

; FILING DATE: 07-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 1579-33

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-116-733-31

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 9

US-08-116-733-32

; Sequence 32, Application US/08116733

; Patent No. 5516632

; GENERAL INFORMATION:

; APPLICANT: PALKER, Thomas J.

; APPLICANT: HAYNES, Barton F.

; TITLE OF INVENTION: SYNTHETIC PEPTIDES

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/116,733

; FILING DATE: 07-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 1579-33

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-116-733-32

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 2 AKK 4

RESULT 10

US-08-116-733-33

; Sequence 33, Application US/08116733

; Patent No. 5516632

; GENERAL INFORMATION:

; APPLICANT: PALKER, Thomas J.

```

; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-33

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```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      5 KPN 7
      |||
Db      4 KPN 6

```

```

RESULT 11
US-08-116-733-37
; Sequence 37, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

```

```

; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-37

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KPN 7
        |||
Db      4 KPN 6

```

```

RESULT 12
US-08-116-733-38
; Sequence 38, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/116,733
;   FILING DATE: 07-SEP-1993
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WILSON, MARY J.
;   REGISTRATION NUMBER: 32,955
;   REFERENCE/DOCKET NUMBER: 1579-33
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703) 816-4000
;   TELEFAX: (703) 816-4100
;   TELEX: 200797 NIXN UR
;   INFORMATION FOR SEQ ID NO: 38:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-116-733-38

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          5 KPN 7
            |||
Db          4 KPN 6

```

RESULT 13

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US-08-116-733-39
; Sequence 39, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.

```

; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-39

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 14

US-08-116-733-40
; Sequence 40, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-40

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 4 KPN 6

RESULT 15

US-08-116-733-41

; Sequence 41, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-41

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
| | |
Db 4 KPN 6

RESULT 16

US-08-167-035-38

; Sequence 38, Application US/08167035

; Patent No. 5618691

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnick, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE

; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: 10036-2711

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/167,035

; FILING DATE: 16-DEC-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7683-062

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-167-035-38

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
 | | |
Db 1 KPN 3

RESULT 17

US-08-428-488-16

; Sequence 16, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = p-Glu."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Position 11 = Met-NH2."
US-08-428-488-16

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8
 |||
Db 4 PNK 6

RESULT 18

US-08-434-120-112

; Sequence 112, Application US/08434120

; Patent No. 5635479

; GENERAL INFORMATION:

; APPLICANT: Baker, Margaret A.

; APPLICANT: Jacob, Leonard S.

; APPLICANT: Maloy, W. Lee

; TITLE OF INVENTION: Treatment of Gynecological

; TITLE OF INVENTION: Malignancies with

; TITLE OF INVENTION: Biologically Active Peptides

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi & Stewart

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: DW4.V2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,120

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/297,950

; FILING DATE:

; APPLICATION NUMBER: US/08/226,108

; FILING DATE:

; APPLICATION NUMBER: US/07/937,462

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Olstein, Elliot M.

; REGISTRATION NUMBER: 24,025

; REFERENCE/DOCKET NUMBER: 421250-194

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 112:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-434-120-112

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 | | |
Db 1 AKK 3

RESULT 19

US-07-958-903A-14

; Sequence 14, Application US/07958903A

; Patent No. 5652214

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.

; APPLICANT: Kauer, James C.

; APPLICANT: Smith, Kevin R.

; APPLICANT: Callison, Kathleen V.

; APPLICANT: Baldino, Frank

; APPLICANT: Neff, Nicola

; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION

; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND

; TITLE OF INVENTION: ANALOGS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/958,903A

; FILING DATE: October 7, 1992

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/361,595

; FILING DATE: June 5, 1989

; APPLICATION NUMBER: 07/534,139

; FILING DATE: June 5, 1990

; APPLICATION NUMBER: 07/869,913

; FILING DATE: April 15, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 02655/003004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-958-903A-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 4 NKP 6

RESULT 20

US-08-208-887A-38
; Sequence 38, Application US/08208887A
; Patent No. 5677421
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Skolnick, Edward Y.
; APPLICANT: Margolis, Benjamin L.
; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: 10036-2711
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,887A
; FILING DATE: 11-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-208-887A-38

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 1 KPN 3

RESULT 21

US-08-465-325-111

; Sequence 111, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-111

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 22

US-08-465-325-122

; Sequence 122, Application US/08465325
; Patent No. 5686563

; GENERAL INFORMATION:

; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:

; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 122:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-122

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3 .
|||
Db 7 AKK 9

RESULT 23

US-08-465-325-123

; Sequence 123, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-123

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 24

US-07-789-184-20

; Sequence 20, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-07-789-184-20

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 PND 11
            |||
Db          8 PND 10

```

RESULT 25

```

US-07-789-184-28
; Sequence 28, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:

```

```

;   LENGTH: 11 amino acids
;   TYPE: AMINO ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   OTHER INFORMATION: /note= "This position is Mpr,
;   OTHER INFORMATION: S-Me Mpr or Mba."
US-07-789-184-28

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 26

US-07-789-184-37

```

; Sequence 37, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/789,184
;   FILING DATE: 19911107
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MURASHIGE, KATE H.
;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 813-5600
;   TELEFAX: (415) 494-0792
;   TELEX: 34-0154
;   INFORMATION FOR SEQ ID NO: 37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids

```

```

;     TYPE:  AMINO ACID
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;     FEATURE:
;     NAME/KEY:  Modified-site
;     LOCATION:  1
;     OTHER INFORMATION:  /note= "This position is Mpr,
;     OTHER INFORMATION:  S-Me Mpr or Mba."
;     FEATURE:
;     NAME/KEY:  Modified-site
;     LOCATION:  3
;     OTHER INFORMATION:  /note= "This position is Cha."
;     FEATURE:
;     NAME/KEY:  Modified-site
;     LOCATION:  4
;     OTHER INFORMATION:  /note= "This position is Cha."
US-07-789-184-37

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 27

US-07-789-184-39

```

; Sequence 39, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
;   APPLICANT:  COUGHLIN, SHAUN R.
;   APPLICANT:  SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES:  223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  MORRISON & FOERSTER
;   STREET:  755 Page Mill Road
;   CITY:  Palo Alto
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/789,184
;   FILING DATE:  19911107
;   CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MURASHIGE, KATE H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  22000-20502.20

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-07-789-184-39

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

RESULT 28

US-07-789-184-52

; Sequence 52, Application US/07789184

; Patent No. 5688768

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; APPLICANT: SCARBOROUGH, ROBERT M.

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

; TITLE OF INVENTION: RELATED PHARMACEUTICALS

; NUMBER OF SEQUENCES: 223

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk


```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/789,184
;   FILING DATE:  19911107
;   CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MURASHIGE, KATE H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 813-5600
;   TELEFAX:  (415) 494-0792
;   TELEX:  34-0154
;   INFORMATION FOR SEQ ID NO:  52:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  AMINO ACID
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  1
;   OTHER INFORMATION:  /note= "This position is Mpr."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is Cha."
US-07-789-184-52

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

RESULT 29

US-07-789-184-54

```

; Sequence 54, Application US/07789184
; Patent No. 5688768
;   GENERAL INFORMATION:
;   APPLICANT:  COUGHLIN, SHAUN R.
;   APPLICANT:  SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES:  223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  MORRISON & FOERSTER
;   STREET:  755 Page Mill Road

```

```

; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-07-789-184-54

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          9 PND 11
            |||
Db          7 PND 9

```

```

RESULT 30
US-07-789-184-181
; Sequence 181, Application US/07789184

```

```

; Patent No. 5688768
; GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MORRISON & FOERSTER
;     STREET: 755 Page Mill Road
;     CITY: Palo Alto
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/789,184
;     FILING DATE: 19911107
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MURASHIGE, KATE H.
;     REGISTRATION NUMBER: 29,959
;     REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 813-5600
;     TELEFAX: (415) 494-0792
;     TELEX: 34-0154
;   INFORMATION FOR SEQ ID NO: 181:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: AMINO ACID
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 3
;       OTHER INFORMATION: /note= "This position is (Cha)."
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US-07-789-184-181

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```

Qy      9 PND 11
      |||
Db      8 PND 10
```

RESULT 31

US-08-462-018-14
 ; Sequence 14, Application US/08462018
 ; Patent No. 5703045
 ; GENERAL INFORMATION:
 ; APPLICANT: Lewis, Michael E.
 ; APPLICANT: Kauer, James C.
 ; APPLICANT: Smith, Kevin R.
 ; APPLICANT: Callison, Kathleen V.
 ; APPLICANT: Baldino, Frank
 ; APPLICANT: Neff, Nicola
 ; APPLICANT: Iqbal, Mohamed
 ; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
 ; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
 ; TITLE OF INVENTION: ANALOGS
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,018
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/958,903
 ; FILING DATE: October 7, 1992
 ; APPLICATION NUMBER: 07/361,595
 ; FILING DATE: June 5, 1989
 ; APPLICATION NUMBER: 07/534,139
 ; FILING DATE: June 5, 1990
 ; APPLICATION NUMBER: 07/869,913
 ; FILING DATE: April 15, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 02655/003005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 US-08-462-018-14

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
|||
Db 4 NKP 6

RESULT 32

US-08-156-552A-17

; Sequence 17, Application US/08156552A

; Patent No. 5726155

; GENERAL INFORMATION:

; APPLICANT: Bokoch, Gary M

; APPLICANT: Curnutte, John T

; TITLE OF INVENTION: REGULATION OF OXIDATIVE BURST USING

; TITLE OF INVENTION: LMWG-DERIVED PEPTIDES AND ANALOGS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5726155th Torrey Pines Road, TPC 8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/156,552A

; FILING DATE: 15-NOV-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/102,944

; FILING DATE: 02-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Logan, April C.

; REGISTRATION NUMBER: 33,950

; REFERENCE/DOCKET NUMBER: SCRF 281.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-156-552A-17

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5
 |||
Db 4 KEK 6

RESULT 33

US-08-475-263-20

; Sequence 20, Application US/08475263

; Patent No. 5759994

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; APPLICANT: SCARBOROUGH, ROBERT M.

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

; TITLE OF INVENTION: RELATED PHARMACEUTICALS

; NUMBER OF SEQUENCES: 223

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave., NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,263

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 22000-20502.03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; TELEX: 90-4030

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 3

; OTHER INFORMATION: /note= "This position is Cha."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 4

; OTHER INFORMATION: /note= "This position is Cha."

US-08-475-263-20

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 8 PND 10

RESULT 34

US-08-475-263-28

; Sequence 28, Application US/08475263

; Patent No. 5759994

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; APPLICANT: SCARBOROUGH, ROBERT M.

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

; TITLE OF INVENTION: RELATED PHARMACEUTICALS

; NUMBER OF SEQUENCES: 223

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave., NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,263

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 22000-20502.03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; TELEX: 90-4030

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note= "This position is Mpr,

; OTHER INFORMATION: S-Me Mpr or Mba."

US-08-475-263-28

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 35

US-08-475-263-37

; Sequence 37, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site

; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-475-263-37

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 36

US-08-475-263-39

; Sequence 39, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,

```

;   OTHER INFORMATION:  S-Me Mpr or Mba."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  11
;   OTHER INFORMATION:  /note= "This position is Y-NH2."
US-08-475-263-39

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 37

US-08-475-263-52

; Sequence 52, Application US/08475263

; Patent No. 5759994

; GENERAL INFORMATION:

; APPLICANT: COUGHLIN, SHAUN R.

; APPLICANT: SCARBOROUGH, ROBERT M.

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

; TITLE OF INVENTION: RELATED PHARMACEUTICALS

; NUMBER OF SEQUENCES: 223

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave., NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/475,263

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 22000-20502.03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

```

;       TELEX: 90-4030
;   INFORMATION FOR SEQ ID NO: 52:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 1
;       OTHER INFORMATION: /note= "This position is Mpr."
;   FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 3
;       OTHER INFORMATION: /note= "This position is Cha."
;   FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 4
;       OTHER INFORMATION: /note= "This position is Cha."
US-08-475-263-52

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 PND 11
            |||
Db          7 PND 9

```

RESULT 38

US-08-475-263-54

```

; Sequence 54, Application US/08475263
; Patent No. 5759994
;   GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 2000 Pennsylvania Ave., NW
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20006-1812
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/475,263
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:

```

```

; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-08-475-263-54

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 39

US-08-475-263-181

```

; Sequence 181, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is (Cha)."
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US-08-475-263-181

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```

Qy      9 PND 11
      |||
Db      8 PND 10
```

RESULT 40

US-08-315-026B-2

```

; Sequence 2, Application US/08315026B
; Patent No. 5763199
; GENERAL INFORMATION:
; APPLICANT: Coller, Barry S.
; TITLE OF INVENTION: PLATELET BLOCKADE ASSAY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 525 University Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301-1900
```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,026B
; FILING DATE: 29-Sep-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 22608-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-7041
; TELEFAX: (415) 324-0638
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-315-026B-2

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

RESULT 41

```

US-08-315-026B-5
; Sequence 5, Application US/08315026B
; Patent No. 5763199
; GENERAL INFORMATION:
; APPLICANT: Coller, Barry S.
; TITLE OF INVENTION: PLATELET BLOCKADE ASSAY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 525 University Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301-1900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/315,026B
; FILING DATE: 29-Sep-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 22608-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-7041
; TELEFAX: (415) 324-0638
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= ""xaa=isoserine""
US-08-315-026B-5

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 PND 11
            |||
Db          7 PND 9

```

RESULT 42

US-08-823-245-14

```

; Sequence 14, Application US/08823245
; Patent No. 5776897

```

; GENERAL INFORMATION:

```

; APPLICANT: Lewis, Michael
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY
; TITLE OF INVENTION: APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
; TITLE OF INVENTION: FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson

```

```

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or
; COMPUTER: 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version
; SOFTWARE: 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,245
; FILING DATE: March 24, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 6, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Creeson, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 02655/003008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-823-245-14

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NKP 9
      |||
Db      4 NKP 6

```

```

RESULT 43
US-08-485-886-20
; Sequence 20, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.

```



```

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-485-886-20

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      8 PND 10

```

```

RESULT 44
US-08-485-886-28

```

```

; Sequence 28, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MORRISON & FOERSTER
;     STREET: 755 Page Mill Road
;     CITY: Palo Alto
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/485,886
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/789,184
;     FILING DATE: 07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: MURASHIGE, KATE H.
;     REGISTRATION NUMBER: 29,959
;     REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 813-5600
;     TELEFAX: (415) 494-0792
;     TELEX: 34-0154
;   INFORMATION FOR SEQ ID NO: 28:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 1
;       OTHER INFORMATION: /note= "This position is Mpr,
;       OTHER INFORMATION: S-Me Mpr or Mba."
US-08-485-886-28

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 45
 US-08-485-886-37
 ; Sequence 37, Application US/08485886
 ; Patent No. 5798248
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,886
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/789,184
 ; FILING DATE: 07-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "This position is Mpr,
 ; OTHER INFORMATION: S-Me Mpr or Mba."
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 3
 ; OTHER INFORMATION: /note= "This position is Cha."
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 4
 ; OTHER INFORMATION: /note= "This position is Cha."
 US-08-485-886-37

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PND 11
|||
Db 7 PND 9

RESULT 46

US-08-485-886-39

; Sequence 39, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,

```

;   OTHER INFORMATION:  S-Me Mpr or Mba."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  11
;   OTHER INFORMATION:  /note= "This position is Y-NH2."
US-08-485-886-39

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

RESULT 47

US-08-485-886-52

```

; Sequence 52, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
;   APPLICANT:  COUGHLIN, SHAUN R.
;   APPLICANT:  SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION:  RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION:  RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES:  223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  MORRISON & FOERSTER
;   STREET:  755 Page Mill Road
;   CITY:  Palo Alto
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/485,886
;   FILING DATE:  07-JUN-1995
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/789,184
;   FILING DATE:  07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  MURASHIGE, KATE H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  22000-20502.20

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-485-886-52

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 48

US-08-485-886-54

```

; Sequence 54, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886

```

```

; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-08-485-886-54

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 49

US-08-485-886-181

```

; Sequence 181, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE:  MORRISON & FOERSTER
;   STREET:    755 Page Mill Road
;   CITY:     Palo Alto
;   STATE:    California
;   COUNTRY:   USA
;   ZIP:      94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:   PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/485,886
;   FILING DATE:   07-JUN-1995
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/789,184
;   FILING DATE:   07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:   MURASHIGE, KATE H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 813-5600
;   TELEFAX:   (415) 494-0792
;   TELEX:    34-0154
;   INFORMATION FOR SEQ ID NO:  181:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:   11 amino acids
;   TYPE:     amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is (Cha)."
```

```

;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is (Cha)."
```

US-08-485-886-181

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```

Qy      9 PND 11
      |||
Db      8 PND 10
```

RESULT 50

US-08-459-568-6

```

; Sequence 6, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
```



```

; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-6

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 EKP 6
      |||
Db      6 EKP 8

```

RESULT 51

US-08-459-568-91

```

; Sequence 91, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700

```

```

;   CITY:  San Diego
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  92122
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/459,568
;   FILING DATE:  02-JUN-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/399,411
;   FILING DATE:  06-MAR-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Campbell, Cathryn A.
;   REGISTRATION NUMBER:  31,815
;   REFERENCE/DOCKET NUMBER:  P-LJ 1264
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (619) 535-9001
;   TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  91:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
US-08-459-568-91

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      4 EKP 6
      |||
Db      6 EKP 8

```

RESULT 52

US-08-796-598-7

```

; Sequence 7, Application US/08796598
; Patent No. 5827659

```

; GENERAL INFORMATION:

```

;   APPLICANT:  PATTERSON, DALE H.
;   APPLICANT:  TARR, GEORGE E.
;   TITLE OF INVENTION:  METHODS AND APPARATUS FOR SEQUENCING
;   TITLE OF INVENTION:  POLYMERS USING MASS SPECTROMETRY.
;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Patent Administrator - Testa, Hurwitz &
;   ADDRESSEE:  Thibeault
;   STREET:  High Street Tower, 125 High Street
;   CITY:  Boston
;   STATE:  MA
;   COUNTRY:  USA
;   ZIP:  02110

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN Esq., Kerry A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SYP-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-796-598-7

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 PNK 8
        |||
Db      4 PNK 6

```

RESULT 53

US-08-399-411-6

```

; Sequence 6, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/399,411
;   FILING DATE: 06-MAR-1995
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Campbell, Cathryn A.
;   REGISTRATION NUMBER: 31,815
;   REFERENCE/DOCKET NUMBER: P-LJ 1264
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
US-08-399-411-6

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 EKP 6
      |||
Db      6 EKP 8

```

```

RESULT 54
US-08-399-411-91
; Sequence 91, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-399-411-91

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 6 EKP 8

RESULT 55

US-08-477-362-20

; Sequence 20, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 20:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 3
;   OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /note= "This position is Cha."
US-08-477-362-20

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      8 PND 10

```

RESULT 56

US-08-477-362-28

```

; Sequence 28, Application US/08477362
; Patent No. 5849507

```

; GENERAL INFORMATION:

```

; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1018

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991

```

; ATTORNEY/AGENT INFORMATION:

```

; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
US-08-477-362-28

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 57

US-08-477-362-37

```

; Sequence 37, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.

```

```

;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 813-5600
;   TELEFAX: (415) 494-0792
;   TELEX: 34-0154
;   INFORMATION FOR SEQ ID NO: 37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   OTHER INFORMATION: /note= "This position is Mpr,
;   OTHER INFORMATION: S-Me Mpr or Mba."
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 3
;   OTHER INFORMATION: /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /note= "This position is Cha."
US-08-477-362-37

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 PND 11
            |||
Db          7 PND 9

```

RESULT 58

US-08-477-362-39

```

; Sequence 39, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/477,362
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/789,184
;   FILING DATE: 07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MURASHIGE, KATE H.
;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 813-5600
;   TELEFAX: (415) 494-0792
;   TELEX: 34-0154
;   INFORMATION FOR SEQ ID NO: 39:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   OTHER INFORMATION: /note= "This position is Mpr,
;   OTHER INFORMATION: S-Me Mpr or Mba."
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 3
;   OTHER INFORMATION: /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 4
;   OTHER INFORMATION: /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 11
;   OTHER INFORMATION: /note= "This position is Y-NH2."
US-08-477-362-39

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

```

RESULT 59
US-08-477-362-52
; Sequence 52, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.

```

```

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-477-362-52

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY          9 PND 11
            |||
Db          7 PND 9

```

RESULT 60
US-08-477-362-54
; Sequence 54, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."

; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-08-477-362-54

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 61

US-08-477-362-181

; Sequence 181, Application US/08477362
; Patent No. 5849507
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

;   TOPOLOGY:  linear
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is (Cha)."
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```

;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is (Cha)."
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US-08-477-362-181

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Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
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Qy          9 PND 11
            |||
Db          8 PND 10
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RESULT 62

US-08-754-773B-2

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; Sequence 2, Application US/08754773B
; Patent No. 5854005
; GENERAL INFORMATION:
;   APPLICANT:  Coller, Barry S.
;   TITLE OF INVENTION:  PLATELET BLOCKADE ASSAY
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Heller Ehrman White & McAuliffe
;   STREET:  525 University Avenue
;   CITY:  Palo Alto
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94301-1900
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/754,773B
;   FILING DATE:  11/20/96
;   CLASSIFICATION:  436
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Schmonsees, William
;   REGISTRATION NUMBER:  31,796
;   REFERENCE/DOCKET NUMBER:  22608-0006
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 324-7041
;   TELEFAX:  (415) 324-0638
; INFORMATION FOR SEQ ID NO:  2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  unknown
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; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-754-773B-2

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 63

US-08-754-773B-5

; Sequence 5, Application US/08754773B
; Patent No. 5854005
; GENERAL INFORMATION:
; APPLICANT: Coller, Barry S.
; TITLE OF INVENTION: PLATELET BLOCKADE ASSAY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 525 University Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301-1900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,773B
; FILING DATE: 11/20/96
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 22608-0006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-7041
; TELEFAX: (415) 324-0638
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= ""xaa=isoserine""
US-08-754-773B-5

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 64

US-08-477-134-20

; Sequence 20, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-477-134-20

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      8 PND 10

```

RESULT 65

US-08-477-134-28

```

; Sequence 28, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154

```



```

; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 1
;   OTHER INFORMATION: /note= "This position is Mpr,
;   OTHER INFORMATION: S-Me Mpr or Mba."
US-08-477-134-28

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

RESULT 66

US-08-477-134-37

```

; Sequence 37, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
;   APPLICANT: COUGHLIN, SHAUN R.
;   APPLICANT: SCARBOROUGH, ROBERT M.
;   TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
;   TITLE OF INVENTION: RELATED PHARMACEUTICALS
;   NUMBER OF SEQUENCES: 223
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/477,134
;   FILING DATE: 07-JUN-1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/789,184
;   FILING DATE: 07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MURASHIGE, KATE H.
;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 813-5600

```

```

; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
US-08-477-134-37

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```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
        |||
Db      7 PND 9

```

RESULT 67

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US-08-477-134-39
; Sequence 39, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995

```

```

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."
US-08-477-134-39

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

```

RESULT 68
US-08-477-134-52
; Sequence 52, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE:  MORRISON & FOERSTER
;   STREET:    755 Page Mill Road
;   CITY:     Palo Alto
;   STATE:    California
;   COUNTRY:   USA
;   ZIP:      94304-1018
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE:   PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/477,134
;   FILING DATE:    07-JUN-1995
;   CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/789,184
;   FILING DATE:    07-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:   MURASHIGE, KATE H.
;   REGISTRATION NUMBER:  29,959
;   REFERENCE/DOCKET NUMBER:  22000-20502.20
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 813-5600
;   TELEFAX:   (415) 494-0792
;   TELEX:    34-0154
;   INFORMATION FOR SEQ ID NO:  52:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:    amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  1
;   OTHER INFORMATION:  /note= "This position is Mpr."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  3
;   OTHER INFORMATION:  /note= "This position is Cha."
;   FEATURE:
;   NAME/KEY:  Modified-site
;   LOCATION:  4
;   OTHER INFORMATION:  /note= "This position is Cha."
US-08-477-134-52

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.3e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 PND 11
      |||
Db      7 PND 9

```

```

RESULT 69
US-08-477-134-54

```

; Sequence 54, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is Cha."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "This position is Y-NH2."

US-08-477-134-54

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 7 PND 9

RESULT 70

US-08-477-134-181

; Sequence 181, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3

; OTHER INFORMATION: /note= "This position is (Cha)."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is (Cha)."
US-08-477-134-181

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 8 PND 10

RESULT 71

US-08-539-005-38

; Sequence 38, Application US/08539005
; Patent No. 5858686
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Skolnick, Edward Y.
; APPLICANT: Margolis, Benjamin L.
; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: 10036-2711
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,005
; FILING DATE: 4-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/167,035
; FILING DATE: 16-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-539-005-38

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 1 KPN 3

RESULT 72

US-08-447-175A-7

; Sequence 7, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; TITLE OF INVENTION: SPECTROMETRY.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESSEE: Thibeault, LLP
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SYP-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-447-175A-7

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8
|||
Db 4 PNK 6

RESULT 73

US-08-538-960-8

; Sequence 8, Application US/08538960
; Patent No. 5872230
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: REGULATION OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,960
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43375.0002/DLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-538-960-8

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 74

US-08-934-222-29

; Sequence 29, Application US/08934222

; Patent No. 5928896

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,222

; FILING DATE: 19-SEPT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-934-222-29

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9

Db |||
 7 NKP 9

RESULT 75
US-08-934-222-108
; Sequence 108, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-108

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NKP 9
 |||

Db

8 NKP 10

Search completed: April 8, 2004, 15:52:13
Job time : 12.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
 (without alignments)
 122.816 Million cell updates/sec

Title: US-09-787-443A-17
 Perfect score: 11
 Sequence: 1 AKKEKPNKPND 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3	27.3	11	2	S07201	physalaemin - frog
2	3	27.3	11	2	D61033	ranatachykinin D -
3	3	27.3	11	2	PD0441	translation elonga
4	2	18.2	11	1	SPHO	substance P - hors
5	2	18.2	11	1	A60654	substance P - guin
6	2	18.2	11	2	A38841	rhodopsin homolog
7	2	18.2	11	2	PQ0682	photosystem I 17.5
8	2	18.2	11	2	C53652	rhlR protein - Pse
9	2	18.2	11	2	A26930	ermG leader peptid
10	2	18.2	11	2	D60409	kassinin-like pept
11	2	18.2	11	2	F60409	substance P-like p
12	2	18.2	11	2	E60409	substance P-like p
13	2	18.2	11	2	S23308	substance P - rain

14	2	18.2	11	2	S23306	substance P - Atla
15	2	18.2	11	2	C60409	kassinin-like pept
16	2	18.2	11	2	S07203	uperolein - frog (
17	2	18.2	11	2	A61033	ranatachykinin A -
18	2	18.2	11	2	S42449	ant1 protein - pha
19	2	18.2	11	2	JQ0395	hypothetical prote
20	2	18.2	11	2	PQ0231	beta-glucosidase (
21	2	18.2	11	2	S66606	quinoline 2-oxidor
22	2	18.2	11	2	A58838	hemolysin - Porphy
23	2	18.2	11	2	B43669	hypothetical prote
24	2	18.2	11	2	PC2372	58K heat shock pro
25	2	18.2	11	2	B41835	translation elonga
26	2	18.2	11	2	S33519	probable secreted
27	2	18.2	11	2	PT0081	protein QA300023 -
28	2	18.2	11	2	PA0028	protein QA300042 -
29	2	18.2	11	2	C59151	protein-tyrosine k
30	2	18.2	11	2	G61497	seed protein ws-23
31	2	18.2	11	2	S19775	wound-induced prot
32	2	18.2	11	2	S71304	amine oxidase (cop
33	2	18.2	11	2	A26120	6-phosphofructokin
34	2	18.2	11	2	S69349	neuropeptide FFami
35	2	18.2	11	2	I41978	calliFMRFamide 9 -
36	2	18.2	11	2	S33300	probable substance
37	2	18.2	11	2	A33571	folliclistatin - bovi
38	2	18.2	11	2	S23926	major glycoprotein
39	2	18.2	11	2	A14454	6-phosphofructokin
40	2	18.2	11	2	PH1376	T antigen variant
41	2	18.2	11	2	S65377	cytochrome-c oxida
42	2	18.2	11	2	PH0939	T-cell receptor be
43	2	18.2	11	2	H84082	hypothetical prote
44	2	18.2	11	4	S19015	hypothetical prote
45	1	9.1	11	1	XAVIBH	bradykinin-potenti
46	1	9.1	11	1	XASNBA	bradykinin-potenti
47	1	9.1	11	1	ECLQ2M	tachykinin II - mi
48	1	9.1	11	1	EOOCC	eledoisin - curled
49	1	9.1	11	1	EOOC	eledoisin - musky
50	1	9.1	11	1	GMROL	leucosulfakinin -
51	1	9.1	11	1	LFTWWE	probable trpEG lea
52	1	9.1	11	2	S66196	alcohol dehydrogen
53	1	9.1	11	2	G42762	proteasome endopep
54	1	9.1	11	2	S68392	H+-transporting tw
55	1	9.1	11	2	A33917	dihydroorotase (EC
56	1	9.1	11	2	B49164	chromogranin-B - r
57	1	9.1	11	2	JN0023	substance P - chic
58	1	9.1	11	2	S32575	ribosomal protein
59	1	9.1	11	2	A40693	transgelin - sheep
60	1	9.1	11	2	S00616	parasporal crystal
61	1	9.1	11	2	S09074	cytochrome P450-4b
62	1	9.1	11	2	A57458	gene Gax protein -
63	1	9.1	11	2	YHRT	morphogenetic neur
64	1	9.1	11	2	YHHU	morphogenetic neur
65	1	9.1	11	2	YHBO	morphogenetic neur
66	1	9.1	11	2	YHXAE	morphogenetic neur
67	1	9.1	11	2	YHJFHY	morphogenetic neur
68	1	9.1	11	2	A61365	phyllokinin - Rohd
69	1	9.1	11	2	B26744	megascalikin -
70	1	9.1	11	2	B60409	kassinin-like pept

71	1	9.1	11	2	S07207	Crinia-angiotensin
72	1	9.1	11	2	B58501	24K kidney and bla
73	1	9.1	11	2	D58502	27K bile and gallb
74	1	9.1	11	2	A58502	38K kidney stone p
75	1	9.1	11	2	C58501	42K bile stone pro
76	1	9.1	11	2	F58501	43.5K bile stone p
77	1	9.1	11	2	S58244	pyrroloquinoline q
78	1	9.1	11	2	S04875	nifS protein - Bra
79	1	9.1	11	2	I41138	acetyl ornithine d
80	1	9.1	11	2	S42587	celF protein - Esc
81	1	9.1	11	2	S35490	type II site-speci
82	1	9.1	11	2	S21127	precorrin methyltr
83	1	9.1	11	2	S70720	trigger factor hom
84	1	9.1	11	2	S33782	acetolactate synth
85	1	9.1	11	2	B39853	LuxC protein - Pho
86	1	9.1	11	2	E60691	phycobilisome 8K l
87	1	9.1	11	2	D60691	phycobilisome 9K l
88	1	9.1	11	2	PC2330	cycloinulooligosac
89	1	9.1	11	2	S14087	parasporal crystal
90	1	9.1	11	2	A44755	20alpha-hydroxyste
91	1	9.1	11	2	E41476	probable antigen 5
92	1	9.1	11	2	A55149	tetracenomycin A2
93	1	9.1	11	2	S19301	endo-1,4-beta-xyla
94	1	9.1	11	2	H54346	pyruvate synthase
95	1	9.1	11	2	S70338	napin small chain
96	1	9.1	11	2	T06383	hypothetical prote
97	1	9.1	11	2	C61497	seed protein ws-18
98	1	9.1	11	2	JQ2307	hypothetical 1.5K
99	1	9.1	11	2	S41747	chaperonin 10 homo
100	1	9.1	11	2	JQ2317	hypothetical 1.5K

ALIGNMENTS

RESULT 1

S07201

physalaemin - frog (*Physalaemus fuscomaculatus*)

C;Species: *Physalaemus fuscomaculatus*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07201

R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of *Physalaemus fuscumaculatus*.

A;Reference number: S07201; MUID:66076612; PMID:5857249

A;Accession: S07201

A;Molecule type: protein

A;Residues: 1-11 <ERS>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8
 | | |
Db 4 PNK 6

RESULT 2

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: D61033; JE0429

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: D61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0429

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
 | | |
Db 1 KPN 3

RESULT 3

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 4 AKK 6

RESULT 4

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 3 KP 4

RESULT 5

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 3 KP 4

RESULT 6

A38841

rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)

N;Alternate names: visual pigment protein

C;Species: *Watasenia scintillans* (sparkling enope)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997

C;Accession: A38841

R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.

Biochim. Biophys. Acta 957, 318-321, 1988

A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.

A;Reference number: PT0063; MUID:89051045; PMID:3191148

A;Accession: A38841

A;Molecule type: protein

A;Residues: 1-11 <SEI>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 2 AK 3

RESULT 7

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in *Nicotiana* spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 7 KE 8

RESULT 8

C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 3 ND 4

RESULT 9

A26930

ermG leader peptide 1 - *Bacillus sphaericus*

C;Species: *Bacillus sphaericus*

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:gl42881; PIDN:AAA22417.1; PID:gl42882

C;Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 2 NK 3

RESULT 10

D60409

kassinin-like peptide K-III - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;

Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: D60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7

||

Db 4 PN 5

RESULT 11

F60409

substance P-like peptide II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;

Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7

||

Db 2 PN 3

RESULT 12

E60409

substance P-like peptide I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7

||

Db 2 PN 3

RESULT 13

S23308

substance P - rainbow trout

C;Species: *Oncorhynchus mykiss* (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
Db 1 KP 2

RESULT 14

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
Db 1 KP 2

RESULT 15

C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 2 PN 3

RESULT 16

S07203

uperolein - frog (*Uperoleia marmorata*)

C;Species: *Uperoleia marmorata*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07203

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.

A;Reference number: S07203; MUID:75131227; PMID:1120493

A;Accession: S07203

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 4 PN 5

RESULT 17

A61033

ranatachykinin A - bullfrog

C;Species: *Rana catesbeiana* (bullfrog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000

C;Accession: A61033; JE0426

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain and intestine.

A;Reference number: A61033

A;Accession: A61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143
A;Accession: JE0426
A;Molecule type: protein
A;Residues: 1-11 <KOZ>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 1 KP 2

RESULT 18

S42449

ant1 protein - phage P7

C;Species: phage P7

C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999

C;Accession: S42449

R;Citron, M.; Schuster, H.

Cell 62, 591-598, 1990

A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.

A;Reference number: S42448; MUID:90335968; PMID:1696181

A;Accession: S42449

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-11 <CIT>

A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 19

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Gen. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:
nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>
A;Cross-references: GB:L18897
A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 20

PQ0231

beta-glucosidase (EC 3.2.1.21) - *Cellvibrio gilvus* (fragment)

C;Species: *Cellvibrio gilvus*

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 07-May-1999

C;Accession: PQ0231

R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.

Agric. Biol. Chem. 55, 2553-2559, 1991

A;Title: Characterization of a beta-glucosidase encoded by a gene from *Cellvibrio gilvus*.

A;Reference number: PQ0231; MUID:92144103; PMID:1368758

A;Accession: PQ0231

A;Molecule type: protein

A;Residues: 1-11 <KAS>

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 10 KP 11

RESULT 21

S66606

quinoline 2-oxidoreductase alpha chain - *Comamonas testosteroni* (fragment)

C;Species: *Comamonas testosteroni*

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from *Comamonas testosteroni* 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 22

A58838

hemolysin - Porphyromonas gingivalis (fragment)

C;Species: Porphyromonas gingivalis

C;Date: 29-Sep-1999 #sequence_revision 29-Sep-1999 #text_change 29-Sep-1999

C;Accession: A58838

R;Deshpande, R.

submitted to the Protein Sequence Database, April 1998

A;Reference number: A58838

A;Accession: A58838

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DES>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 4 PN 5

RESULT 23

B43669

hypothetical protein (rhdA 5' region) - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C;Accession: B43669

R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.

J. Bacteriol. 173, 2751-2760, 1991

A;Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasmically localized protein with sequence similarity to rhodanese.

A;Reference number: A43669; MUID:91210163; PMID:1708376

A;Accession: B43669

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <LAU>

A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 6 AK 7

RESULT 24

PC2372

58K heat shock protein groEL [similarity] - *Bacillus cereus* (strain ts-4) (fragment)

C;Species: *Bacillus cereus*

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 25

B41835

translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997

C;Accession: B41835

R;Mitchell, C.; Morris, P.W.; Vary, J.C.

J. Bacteriol. 174, 2474-2477, 1992

A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus subtilis*.

A;Reference number: A41835; MUID:92210489; PMID:1556067

A;Accession: B41835

A;Molecule type: protein

A;Residues: 1-11 <MIT>

A;Note: this protein is phosphorylated during stationary phase but not during exponential growth

C;Keywords: phosphoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
||
Db 4 EK 5

RESULT 26

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: Acholeplasma laidlawii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999
C;Accession: S33519
R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL Data Library, June 1993
A;Description: Sequence regions from Acholeplasma laidlawii which restore export
of beta-lactamase in Escherichia coli.
A;Reference number: S33518
A;Accession: S33519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <BOY>
A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 27

PT0081
protein QA300023 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C;Accession: PT0081
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and
standardization of the gel patterns.
A;Reference number: PN0173
A;Accession: PT0081
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: Leaf
C;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 2 KE 3

RESULT 28

PA0028
protein QA300042 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0028
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0028

A;Molecule type: protein

A;Residues: 1-11 <KAM>

A;Experimental source: seed

C;Keywords: seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7

||

Db 8 PN 9

RESULT 29

C59151

protein-tyrosine kinase (EC 2.7.1.112) - jack bean (fragment)

C;Species: Canavalia ensiformis (jack bean)

C;Date: 07-Dec-1999 #sequence_revision 07-Dec-1999 #text_change 04-Feb-2000

C;Accession: C59151

R;Oliveira, A.E.A.; Machado, O.L.T.; Gomes, V.M.; Xavier-Neto, J.; Pereira, A.C.P.; Vieira, J.G.H.; Fernandes, K.V.S.; Xavier-Filho, J.

Protein Pept. Lett. 6, 15-21, 1999

A;Title: Jack bean seed coat contains a protein with complete sequence homology to bovine insulin.

A;Reference number: A59151

A;Accession: C59151

A;Molecule type: protein

A;Residues: 1-11 <MAC>

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11

||

Db 2 ND 3

RESULT 30

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HIR>
C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 31

S19775

wound-induced protein - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773

A;Accession: S19775

A;Molecule type: mRNA

A;Residues: 1-11 <PAR>

A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 32

S71304

amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)

C;Species: Aspergillus niger

C;Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999

C;Accession: S71304

R;Frebort, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asano, Y.; Kato, Y.; Matsushita, K.; Toyama, H.; Kumagai, H.; Adachi, O.
Eur. J. Biochem. 237, 255-265, 1996

A;Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the mycelia of Aspergillus niger AKU 3302: purification, characterization, cDNA cloning and sequencing.

A;Reference number: S71303; MUID:96203933; PMID:8620882

A;Accession: S71304

A;Molecule type: protein

A;Residues: 1-11 <FRE>

C;Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinone

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 1 ND 2

RESULT 33

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 34

S69349

neuropeptide FFamide - great pond snail

C;Species: Lymnaea stagnalis (great pond snail)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999

C;Accession: S69349

R;Li, K.W.; El Filali, Z.; van Golen, F.A.; Geraerts, W.P.M.

Eur. J. Biochem. 229, 70-72, 1995

A;Title: Identification of a novel amide peptide, GLTPNMNSLFF-NH(2), involved in the control of vas deferens motility in Lymnaea stagnalis.

A;Reference number: S69349; MUID:95262689; PMID:7744051

A;Accession: S69349

A;Molecule type: protein

A;Residues: 1-11 <LIK>

A;Experimental source: penis complex

C;Function:

A;Description: enhances the contraction frequency and contraction amplitude of the vas deferens

A;Note: control of male reproductive behavior

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 4 PN 5

RESULT 35

I41978

calliFMRFamide 9 - bluebottle fly (*Calliphora vomitoria*)

C;Species: *Calliphora vomitoria*

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C;Accession: I41978

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (designated calliFMRFamides) from the blowfly *Calliphora vomitoria*.

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: I41978

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DUV>

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 6 ND 7

RESULT 36

S33300

probable substance P - smaller spotted catshark

C;Species: *Scyliorhinus canicula* (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, *Scyliorhinus canicula*.

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAV>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 1 KP 2

RESULT 37

A33571

follistatin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993

C;Accession: A33571

R;Gospodarowicz, D.; Lau, K.

Biochem. Biophys. Res. Commun. 165, 292-298, 1989

A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follistatin.

A;Reference number: A33571; MUID:90073725; PMID:2590228

A;Accession: A33571

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 8 AK 9

RESULT 38

S23926

major glycoprotein PAS-6 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999

C;Accession: S23926

R;Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A;Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from bovine milk fat globule membrane.

A;Reference number: S23926; MUID:92353107; PMID:1643094

A;Accession: S23926

A;Molecule type: protein

A;Residues: 1-11 <KIM>

C;Keywords: glycoprotein; milk; blocked amino end

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 4 NK 5

RESULT 39

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993

C;Accession: A14454

R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.

Biochem. Soc. Trans. 7, 721-723, 1979

A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.

A;Reference number: A14454; MUID:80004524; PMID:157899

A;Accession: A14454

A;Molecule type: protein

A;Residues: 1-11 <FOR>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 40

PH1376

T antigen variant K-3 - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C;Accession: PH1376

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 5 NK 6

RESULT 41

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C;Accession: S65377

R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

||

Db 3 AK 4

RESULT 42

PH0939

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0939

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0939

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 5 KP 6

RESULT 43

H84082

hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: H84082
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: H84082
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-11 <STO>
 A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1; GSPDB:GN00137
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH3464

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
 ||
 Db 4 KE 5

RESULT 44

S19015
 hypothetical protein 11 *ruvC-yebC* intergenic region - *Escherichia coli*
 C;Species: *Escherichia coli*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: S19015
 R;Sharples, G.J.; Lloyd, R.G.
 J. Bacteriol. 173, 7711-7715, 1991
 A;Title: Resolution of Holliday junctions in *Escherichia coli*: identification of the *ruvC* gene product as a 19-kilodalton protein.
 A;Reference number: S19013; MUID:92041688; PMID:1657895
 A;Accession: S19015
 A;Molecule type: DNA
 A;Residues: 1-11 <SHA>
 A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174
 C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 4 AK 5

RESULT 45

XAVIBH
 bradykinin-potentiating peptide - *halys viper*

N;Alternate names: BPP
 C;Species: Agkistrodon halys (halys viper)
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994
 C;Accession: JC0002
 R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
 Peptides 6, 339-342, 1985
 A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).
 A;Reference number: JC0002; MUID:86177022; PMID:3008123
 A;Accession: JC0002
 A;Molecule type: protein
 A;Residues: 1-11 <CHI>
 C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 4 P 4

RESULT 46

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)
 C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
 C;Accession: A01254
 R;Kato, H.; Suzuki, T.
 Proc. Jpn. Acad. 46, 176-181, 1970
 A;Reference number: A01254
 A;Accession: A01254
 A;Molecule type: protein
 A;Residues: 1-11 <KAT>
 A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties
 C;Superfamily: bradykinin-potentiating peptide
 C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 8 K 8

RESULT 47

ECLQ2M

tachykinin II - migratory locust

C;Species: *Locusta migratoria* (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.

FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 48

EOOCC

eledoisin - curled octopus

C;Species: *Eledone cirrosa*, *Ozaena cirrosa* (curled octopus)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of *Eledone*.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 49

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 50

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 51

LFTWWE

probable trpEG leader peptide - *Thermus aquaticus*

C;Species: *Thermus aquaticus*

C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C;Accession: S03315

R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.

A;Reference number: S03315; MUID:89000781; PMID:2844259

A;Accession: S03315

A;Molecule type: DNA

A;Residues: 1-11 <SAT>

A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A;Note: the source is designated as *Thermus thermophilus* HB8

C;Genetics:

A;Gene: trpL

C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 52

S66196

alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)

C;Species: *Gadus* sp. (cod)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998

C;Accession: S66196

R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;

Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66196

A;Molecule type: protein

A;Residues: 1-11 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 6 A 6

RESULT 53

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

|

Db 8 K 8

RESULT 54

S68392

H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - *Chlamydomonas reinhardtii* chloroplast (fragment)

N;Alternate names: ATP synthase chain I

C;Species: chloroplast *Chlamydomonas reinhardtii*

C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002

C;Accession: S68392

R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995

A;Title: Isolation of CF(0)CF(1) from *Chlamydomonas reinhardtii* cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.

A;Reference number: S68388; MUID:96128220; PMID:8543042

A;Accession: S68392

A;Molecule type: protein

A;Residues: 1-11 <FIE>

A;Experimental source: strain CW15

C;Genetics:

A;Genome: chloroplast

C;Superfamily: H+-transporting ATP synthase protein 6

C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4

Db |
 1 E 1

RESULT 55

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
Db 2 E 2

RESULT 56

B49164

chromogranin-B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C;Accession: B49164

R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.

A;Reference number: A49164; MUID:92063871; PMID:1954895

A;Accession: B49164

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NIE>

A;Note: sequence extracted from NCBI backbone (NCBIP:66370)

C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 1 P 1

RESULT 57

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 58

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: plastid Conopholis americana (squawroot)

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.

Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: Escherichia coli ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 11 E 11

RESULT 59

A40693

transgelin - sheep (fragment)

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molecule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 60

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)

N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C;Species: *Bacillus thuringiensis*

C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996

C;Accession: S00616

R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 232, 249-251, 1988

A;Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.

A;Reference number: S00615

A;Accession: S00616

A;Molecule type: protein

A;Residues: 1-11 <CHE>

C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).

C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 61

S09074

cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999

C;Accession: S09074

R;Imaoka, S.; Terano, Y.; Funae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.

A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074

A;Molecule type: protein

A;Residues: 1-11 <IMA>

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 4 P 4

RESULT 62

A57458

gene Gax protein - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999

C;Accession: A57458

R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.

Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S79168; NID:g1050991

C;Genetics:
A;Gene: Gax
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 2 E 2

RESULT 63

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 64

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C;Accession: B01427; A01427
 R;Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
 A;Reference number: A93266; MUID:82035850; PMID:7290191
 A;Accession: B01427
 A;Molecule type: protein
 A;Residues: 1-11 <BOD>
 R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A;Reference number: A91296; MUID:82050803; PMID:7297679
 A;Contents: annotation; synthesis
 A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
 C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
 C;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 2 P 2

RESULT 65

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: C01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6

|

Db 2 P 2

RESULT 66

YHXAE

morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)

N;Alternate names: head activator

C;Species: *Anthopleura elegantissima*

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: A93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6

|

Db 2 P 2

RESULT 67

YHJFHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6

|

Db 2 P 2

RESULT 68

A61365

phyllokinin - Rohde's leaf frog

N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61365

R;Anastasi, A.; Bertaccini, G.; Erspamer, V.

Br. J. Pharmacol. 27, 479-485, 1966

A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.

A;Reference number: A61365; MUID:67179312; PMID:5970899

A;Accession: A61365

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: sulfoprotein
F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 69

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 70

B60409

kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: B60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Note: this peptide was also found in a deamidated form
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 71

S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C;Species: Crinia georgiana

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000

C;Accession: S07207

R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979

A;Title: Amino acid composition and sequence of crinia-angiotensin, an
angiotensin II-like endecapeptide from the skin of the Australian frog Crinia
georgiana.

A;Reference number: S07207; MUID:80024575; PMID:488254

A;Accession: S07207

A;Molecule type: protein

A;Residues: 1-11 <ERS>

C;Superfamily: unassigned animal peptides

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 72

B58501

24K kidney and bladder stone protein 2 - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C;Accession: B58501

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: B58501

A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-11 <BIN>
A;Experimental source: human kidney and bladder stones

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 73

D58502

27K bile and gallbladder stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C;Accession: D58502

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: D58502

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

A;Experimental source: human bile and gallbladder stones

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 6 D 6

RESULT 74

A58502

38K kidney stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C;Accession: A58502

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: A58502

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

A;Experimental source: human kidney stone containing Ca ox.mono and dihyd, 1% struvite, CaPO4 carbonate & hydrox., and 4% protein

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 75

C58501

42K bile stone protein - unidentified bacterium (fragment)

C;Species: unidentified bacterium

C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C;Accession: C58501

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A;Description: The proteins of kidney and gallbladder stones.

A;Reference number: A58501

A;Accession: C58501

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

A;Experimental source: human bile with stones

A;Note: tentative identification of 1-Gly

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 6 P 6

Search completed: April 8, 2004, 15:49:27

Job time : 8.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-17
Perfect score: 11
Sequence: 1 AKKEKPNKPND 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications_AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4	36.4	11	9	US-09-879-936-10	Sequence 10, Appl
2	4	36.4	11	10	US-09-876-904A-237	Sequence 237, App
3	4	36.4	11	10	US-09-876-904A-354	Sequence 354, App
4	3	27.3	11	9	US-09-739-936-5	Sequence 5, Appli
5	3	27.3	11	9	US-09-984-056-86	Sequence 86, Appl
6	3	27.3	11	9	US-09-833-079-2	Sequence 2, Appli
7	3	27.3	11	9	US-09-833-079-17	Sequence 17, Appl
8	3	27.3	11	9	US-09-791-378-60	Sequence 60, Appl
9	3	27.3	11	9	US-09-984-057-86	Sequence 86, Appl
10	3	27.3	11	9	US-09-826-290-86	Sequence 86, Appl
11	3	27.3	11	9	US-09-826-290-119	Sequence 119, App
12	3	27.3	11	9	US-09-826-290-246	Sequence 246, App
13	3	27.3	11	10	US-09-791-393-96	Sequence 96, Appl
14	3	27.3	11	10	US-09-791-389-96	Sequence 96, Appl
15	3	27.3	11	10	US-09-906-393A-9	Sequence 9, Appli
16	3	27.3	11	10	US-09-876-904A-200	Sequence 200, App
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18	3	27.3	11	10	US-09-876-904A-434	Sequence 434, App
19	3	27.3	11	10	US-09-876-904A-591	Sequence 591, App
20	3	27.3	11	10	US-09-876-904A-597	Sequence 597, App
21	3	27.3	11	10	US-09-820-053A-113	Sequence 113, App
22	3	27.3	11	10	US-09-820-053A-139	Sequence 139, App
23	3	27.3	11	10	US-09-978-309A-49	Sequence 49, Appl
24	3	27.3	11	10	US-09-978-309A-84	Sequence 84, Appl
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26	3	27.3	11	12	US-10-398-104-210	Sequence 210, App
27	3	27.3	11	12	US-10-601-837-219	Sequence 219, App
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31	3	27.3	11	14	US-10-115-365-28	Sequence 28, Appl
32	3	27.3	11	14	US-10-115-365-29	Sequence 29, Appl
33	3	27.3	11	14	US-10-075-869-26	Sequence 26, Appl
34	3	27.3	11	14	US-10-109-171-113	Sequence 113, App
35	3	27.3	11	14	US-10-109-171-139	Sequence 139, App
36	3	27.3	11	14	US-10-197-954-117	Sequence 117, App
37	3	27.3	11	14	US-10-079-167-8	Sequence 8, Appli
38	3	27.3	11	14	US-10-355-975-33	Sequence 33, Appl
39	3	27.3	11	14	US-10-116-212-28	Sequence 28, Appl
40	3	27.3	11	14	US-10-116-212-29	Sequence 29, Appl
41	3	27.3	11	14	US-10-226-629A-22	Sequence 22, Appl
42	3	27.3	11	14	US-10-226-629A-36	Sequence 36, Appl
43	3	27.3	11	14	US-10-020-269-25	Sequence 25, Appl
44	3	27.3	11	14	US-10-020-269-26	Sequence 26, Appl
45	3	27.3	11	14	US-10-020-269-34	Sequence 34, Appl
46	3	27.3	11	14	US-10-105-232-86	Sequence 86, Appl
47	3	27.3	11	14	US-10-105-232-379	Sequence 379, App
48	3	27.3	11	14	US-10-189-437-86	Sequence 86, Appl
49	3	27.3	11	14	US-10-189-437-366	Sequence 366, App
50	3	27.3	11	15	US-10-376-121A-31	Sequence 31, Appl
51	3	27.3	11	15	US-10-366-493-26	Sequence 26, Appl
52	3	27.3	11	15	US-10-285-394-292	Sequence 292, App
53	3	27.3	11	16	US-10-264-309-93	Sequence 93, Appl
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55	2	18.2	11	8	US-08-450-842-45	Sequence 45, Appl
56	2	18.2	11	8	US-08-891-525-2	Sequence 2, Appli

57	2	18.2	11	8	US-08-452-843A-15	Sequence 15, Appl
58	2	18.2	11	8	US-08-841-636A-28	Sequence 28, Appl
59	2	18.2	11	8	US-08-464-363-27	Sequence 27, Appl
60	2	18.2	11	8	US-08-344-824-44	Sequence 44, Appl
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62	2	18.2	11	9	US-09-341-643-1	Sequence 1, Appli
63	2	18.2	11	9	US-09-778-231-1	Sequence 1, Appli
64	2	18.2	11	9	US-09-729-402-3	Sequence 3, Appli
65	2	18.2	11	9	US-09-827-949-21	Sequence 21, Appl
66	2	18.2	11	9	US-09-802-077-14	Sequence 14, Appl
67	2	18.2	11	9	US-09-802-077-15	Sequence 15, Appl
68	2	18.2	11	9	US-09-802-077-33	Sequence 33, Appl
69	2	18.2	11	9	US-09-802-077-34	Sequence 34, Appl
70	2	18.2	11	9	US-09-758-318-8	Sequence 8, Appli
71	2	18.2	11	9	US-09-802-096-14	Sequence 14, Appl
72	2	18.2	11	9	US-09-802-096-15	Sequence 15, Appl
73	2	18.2	11	9	US-09-802-096-33	Sequence 33, Appl
74	2	18.2	11	9	US-09-802-096-34	Sequence 34, Appl
75	2	18.2	11	9	US-09-850-373-1	Sequence 1, Appli
76	2	18.2	11	9	US-09-828-592-7	Sequence 7, Appli
77	2	18.2	11	9	US-09-828-592-10	Sequence 10, Appl
78	2	18.2	11	9	US-09-814-569-2	Sequence 2, Appli
79	2	18.2	11	9	US-09-765-527-155	Sequence 155, App
80	2	18.2	11	9	US-09-765-527-206	Sequence 206, App
81	2	18.2	11	9	US-09-765-527-208	Sequence 208, App
82	2	18.2	11	9	US-09-765-527-225	Sequence 225, App
83	2	18.2	11	9	US-09-765-527-228	Sequence 228, App
84	2	18.2	11	9	US-09-765-527-229	Sequence 229, App
85	2	18.2	11	9	US-09-780-070-22	Sequence 22, Appl
86	2	18.2	11	9	US-09-780-070-25	Sequence 25, Appl
87	2	18.2	11	9	US-09-780-070-37	Sequence 37, Appl
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93	2	18.2	11	9	US-09-823-649A-15	Sequence 15, Appl
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95	2	18.2	11	9	US-09-823-649A-18	Sequence 18, Appl
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99	2	18.2	11	9	US-09-735-279-35	Sequence 35, Appl
100	2	18.2	11	9	US-09-096-749A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
 US-09-879-936-10
 ; Sequence 10, Application US/09879936
 ; Patent No. US20020045564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Eyk, Jennifer E.
 ; APPLICANT: Mak, Alan S.
 ; APPLICANT: Cote, Graham P.


```

; TITLE OF INVENTION: Methods of Modulating Muscle Contraction
; FILE REFERENCE: 1997-021-03US
; CURRENT APPLICATION NUMBER: US/09/879,936
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/050,478
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/089,505
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon
; NAME/KEY: PEPTIDE
; LOCATION: (11)
; OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-879-936-10

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Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches      4; Conservative    0; Mismatches      0; Indels      0; Gaps      0;

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Qy      1 AKKE 4
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Db      7 AKKE 10

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RESULT 2

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US-09-876-904A-237
; Sequence 237, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-237

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Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
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Db 7 KKEK 10

RESULT 3

US-09-876-904A-354

; Sequence 354, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)
US-09-876-904A-354

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
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Db 7 KKEK 10

RESULT 4

US-09-739-936-5

; Sequence 5, Application US/09739936
; Patent No. US20020058246A1
; GENERAL INFORMATION:
; APPLICANT: Markvardsen, Peter
; Bjornvad, Mads Eskelund
; Mikkelsen, Frank
; Diderichsen, Borge
; TITLE OF INVENTION: Phage Display For Detergent
Enzyme Activity
; NUMBER OF SEQUENCES: 6

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;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: No. US20020058246A1o No. US20020058246A1disk of No.
US20020058246A1th America, Inc.
;      STREET: 405 Lexington Avenue
;      CITY: New York
;      STATE: NY
;      COUNTRY: USA
;      ZIP: 10174
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: DOS
;      SOFTWARE: FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/739,936
;      FILING DATE: 18-Dec-2000
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/017,612
;      FILING DATE: 29-JAN-1998
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Lambiris, Elias J
;      REGISTRATION NUMBER: 33,728
;      REFERENCE/DOCKET NUMBER: 4542.204-US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 212-867-0123
;      TELEFAX: 212-878-9655
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: No. US20020058246A1e
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-739-936-5

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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      3 KEK 5
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Db      5 KEK 7

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RESULT 5
US-09-984-056-86
; Sequence 86, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26

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; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-056-86

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
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Db 4 EKP 6

RESULT 6

US-09-833-079-2

; Sequence 2, Application US/09833079
; Patent No. US20020142008A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; APPLICANT: SCHMIDT, M. ALEXANDER
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USE
; FILE REFERENCE: 050939/0104
; CURRENT APPLICATION NUMBER: US/09/833,079
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-833-079-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
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Db

8 AKK 10

RESULT 7

US-09-833-079-17

; Sequence 17, Application US/09833079
; Patent No. US20020142008A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; APPLICANT: SCHMIDT, M. ALEXANDER
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USE
; FILE REFERENCE: 050939/0104
; CURRENT APPLICATION NUMBER: US/09/833,079
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-833-079-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AKK 3

|||

Db

8 AKK 10

RESULT 8

US-09-791-378-60

; Sequence 60, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT
OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-60

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
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Db 1 EKP 3

RESULT 9

US-09-984-057-86

; Sequence 86, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-057-86

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
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Db 4 EKP 6

RESULT 10

US-09-826-290-86

; Sequence 86, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri

```
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: homo sapien
US-09-826-290-86
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          4 EKP 6
            |||
Db          1 EKP 3
```

RESULT 11

US-09-826-290-119

```
; Sequence 119, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
```

; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-119

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 1 EKP 3

RESULT 12

US-09-826-290-246

; Sequence 246, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 11

; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-246

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 1 EKP 3

RESULT 13

US-09-791-393-96

; Sequence 96, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
(BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-96

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 1 EKP 3

RESULT 14

US-09-791-389-96

; Sequence 96, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri

```

; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder
(BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-96

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 EKP 6
      |||
Db      1 EKP 3

```

```

RESULT 15
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 16

US-09-876-904A-200
; Sequence 200, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-200

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 17

US-09-876-904A-273
; Sequence 273, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:
; OTHER INFORMATION: Recombination repair protein 1
US-09-876-904A-273

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 7 KKE 9

RESULT 18
US-09-876-904A-434
; Sequence 434, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 434
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:
; OTHER INFORMATION: Drosophila ultrabiothorax protein (from the
; OTHER INFORMATION: conserved 61 amino acid homeodomain segment only).
US-09-876-904A-434

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 8 KKE 10

RESULT 19

US-09-876-904A-591
 ; Sequence 591, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 591
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Trout testis H1 (194
 aa).
 US-09-876-904A-591

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred: No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 1 AKK 3

RESULT 20
 US-09-876-904A-597
 ; Sequence 597, Application US/09876904A
 ; Publication No. US20030072794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOULIKAS, TENI
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
 THERAPEUTIC
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
 PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 597
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Parechinus angulosus

; FEATURE:
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-597

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 21

US-09-820-053A-113
; Sequence 113, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-113

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 22

US-09-820-053A-139
; Sequence 139, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-139

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 23

US-09-978-309A-49

; Sequence 49, Application US/09978309A

; Publication No. US20030100490A1

; GENERAL INFORMATION:

; APPLICANT: Cruz, Tony

; APPLICANT: Pastrak, Aleksandra

; APPLICANT: Turley, Eva A.

; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response
to

; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated
by

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; FILE REFERENCE: 033352-010

; CURRENT APPLICATION NUMBER: US/09/978,309A

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 09/685,010

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: US 09/541,522

; PRIOR FILING DATE: 2000-04-03

; PRIOR APPLICATION NUMBER: US 60/127,457

; PRIOR FILING DATE: 1999-04-01

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-978-309A-49

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5
|||
Db 5 KEK 7

RESULT 24

US-09-978-309A-84

; Sequence 84, Application US/09978309A
 ; Publication No. US20030100490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cruz, Tony
 ; APPLICANT: Pastrak, Aleksandra
 ; APPLICANT: Turley, Eva A.
 ; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response
 to
 ; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated
 by
 ; TITLE OF INVENTION: Hyaladherin and Hyaluronans
 ; FILE REFERENCE: 033352-010
 ; CURRENT APPLICATION NUMBER: US/09/978,309A
 ; CURRENT FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: US 09/685,010
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: US 09/541,522
 ; PRIOR FILING DATE: 2000-04-03
 ; PRIOR APPLICATION NUMBER: US 60/127,457
 ; PRIOR FILING DATE: 1999-04-01
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 84
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-978-309A-84

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5
 |||
 Db 5 KEK 7

RESULT 25

US-09-854-248-20

; Sequence 20, Application US/09854248
 ; Publication No. US20030175247A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salgaller, Michael L.
 ; APPLICANT: Boynton, Alton L.
 ; TITLE OF INVENTION: METHOD TO INCREASE CLASS I PRESENTATION OF EXOGENOUS
 ; TITLE OF INVENTION: ANTIGENS BY HUMAN DENDRITIC CELLS
 ; FILE REFERENCE: 20093-8-1US
 ; CURRENT APPLICATION NUMBER: US/09/854,248
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/203,758
 ; PRIOR FILING DATE: 2000-05-12
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-248-20

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 9 KKE 11

RESULT 26

US-10-398-104-210
; Sequence 210, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-210

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PND 11
|||
Db 8 PND 10

RESULT 27

US-10-601-837-219
; Sequence 219, Application US/10601837
; Publication No. US20040053309A1

```

; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment
of Kidney
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 219
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-219

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          5 KPN 7
            |||
Db          3 KPN 5

```

```

RESULT 28
US-10-108-795-28
; Sequence 28, Application US/10108795
; Publication No. US20030033633A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/108,795
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide

```

; OTHER INFORMATION: internal peptide
US-10-108-795-28

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 29

US-10-108-795-29

; Sequence 29, Application US/10108795
; Publication No. US20030033633A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/108,795
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-108-795-29

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 30

US-10-091-135-9

; Sequence 9, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-091-135-9

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
|||
Db 2 KPN 4

RESULT 31

US-10-115-365-28

; Sequence 28, Application US/10115365
; Publication No. US20030074694A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/115,365
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-115-365-28

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 32

US-10-115-365-29

; Sequence 29, Application US/10115365
 ; Publication No. US20030074694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hemmings, Brian A
 ; APPLICANT: Millward, Thomas A
 ; TITLE OF INVENTION: Calcium Regulated Kinase
 ; FILE REFERENCE: 30110
 ; CURRENT APPLICATION NUMBER: US/10/115,365
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 09/133,062
 ; PRIOR FILING DATE: 1998-08-12
 ; PRIOR APPLICATION NUMBER: GB 9717499.9
 ; PRIOR FILING DATE: 1998-08-19
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 29
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
 ; OTHER INFORMATION: internal peptide

US-10-115-365-29

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
 Db 3 AKK 5

RESULT 33

US-10-075-869-26

; Sequence 26, Application US/10075869
 ; Publication No. US20030104622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robbins, Paul D.
 ; APPLICANT: Mi, Zhibao
 ; APPLICANT: Frizzell, Raymond
 ; APPLICANT: Glorioso, Joseph C.
 ; APPLICANT: Gambotto, Andrea
 ; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
 ; TITLE OF INVENTION: FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR
 TRANSPORT
 ; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
 ; FILE REFERENCE: AP32573-AAA 072396.0237
 ; CURRENT APPLICATION NUMBER: US/10/075,869
 ; CURRENT FILING DATE: 2002-02-13
 ; PRIOR APPLICATION NUMBER: 60/151,980
 ; PRIOR FILING DATE: 1999-09-01
 ; PRIOR APPLICATION NUMBER: 60/188,944

; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-10-075-869-26

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 4 AKK 6

RESULT 34

US-10-109-171-113
; Sequence 113, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-10-109-171-113

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 35

US-10-109-171-139
; Sequence 139, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:

```
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (11)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-139
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          1 AKK 3
            |||
Db          8 AKK 10
```

RESULT 36

```
US-10-197-954-117
; Sequence 117, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K"ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 117
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: 11
;   FEATURE:
```

; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa is pyroglutamic acid
US-10-197-954-117

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8
|||
Db 4 PNK 6

RESULT 37

US-10-079-167-8

; Sequence 8, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-8

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5
|||
Db 5 KEK 7

RESULT 38

US-10-355-975-33

; Sequence 33, Application US/10355975
 ; Publication No. US20030162277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Virca, G. Duke
 ; APPLICANT: Martin, Unja
 ; APPLICANT: Anderson, Dirk M.
 ; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
 ; FILE REFERENCE: 2923-A
 ; CURRENT APPLICATION NUMBER: US/10/355,975
 ; CURRENT FILING DATE: 2003-01-30
 ; PRIOR APPLICATION NUMBER: US/09/579,664B
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide

US-10-355-975-33

Query Match 27.3%; Score 3; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
 |||
 Db 3 KKE 5

RESULT 39

US-10-116-212-28

; Sequence 28, Application US/10116212
 ; Publication No. US20030163844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hemmings, Brian A
 ; APPLICANT: Millward, Thomas A
 ; TITLE OF INVENTION: Calcium Regulated Kinase
 ; FILE REFERENCE: 30110
 ; CURRENT APPLICATION NUMBER: US/10/116,212
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: US/09/133,062
 ; PRIOR FILING DATE: 1998-08-12
 ; PRIOR APPLICATION NUMBER: GB 9717089.8
 ; PRIOR FILING DATE: 1997-08-12
 ; PRIOR APPLICATION NUMBER: GB 9717499.9
 ; PRIOR FILING DATE: 1998-08-19
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 28
 ; LENGTH: 11
 ; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-116-212-28

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 40

US-10-116-212-29

; Sequence 29, Application US/10116212
; Publication No. US20030163844A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/116,212
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide

US-10-116-212-29

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 41

US-10-226-629A-22

; Sequence 22, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Equine infectious anemia virus
US-10-226-629A-22

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 8 KKE 10

RESULT 42
US-10-226-629A-36
; Sequence 36, Application US/10226629A
; Publication No. US20030166504A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Equine infectious anemia virus
US-10-226-629A-36

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4

Db |||
 9 KKE 11

RESULT 43

US-10-020-269-25

; Sequence 25, Application US/10020269
; Publication No. US20030175310A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/10/020,269
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/023,921
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-020-269-25

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
 |||
Db 9 KKE 11

RESULT 44

US-10-020-269-26

; Sequence 26, Application US/10020269
; Publication No. US20030175310A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/10/020,269
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/023,921
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-020-269-26

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KEK 5
|||
Db 9 KEK 11

RESULT 45

US-10-020-269-34
; Sequence 34, Application US/10020269
; Publication No. US20030175310A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/10/020,269
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/023,921
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-020-269-34

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 46

US-10-105-232-86
; Sequence 86, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232

; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-232-86

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 4 EKP 6

RESULT 47

US-10-105-232-379

; Sequence 379, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 379
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-379

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 1 KKE 3

RESULT 48

US-10-189-437-86

; Sequence 86, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 86
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-437-86

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 4 EKP 6

RESULT 49

US-10-189-437-366

; Sequence 366, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 366
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-366

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKE 4
|||
Db 1 KKE 3

RESULT 50

US-10-376-121A-31

; Sequence 31, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990


```

; ATTORNEY/AGENT INFORMATION:
;     NAME: Pabst, Patrea L.
;     REGISTRATION NUMBER: 31,284
;     REFERENCE/DOCKET NUMBER: OMRf114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404)-817-8473
;     TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 31:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 11 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FEATURE:
;         NAME/KEY: Binding-site
;         LOCATION: 1..8
;     SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-376-121A-31

```

```

Query Match          27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 KEK 5
      |||
Db      7 KEK 9

```

RESULT 51

US-10-366-493-26

```

; Sequence 26, Application US/10366493
; Publication No. US20030219826A1

```

; GENERAL INFORMATION:

```

; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Gambotto, Andrea
; APPLICANT: Mai, Jeffrey C.
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND
CYTOPLASMIC AND /OR
; TITLE OF INVENTION: NUCLEAR TRANSPORT
; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
; FILE REFERENCE: AP32573-A-A-A-A 072396.0246
; CURRENT APPLICATION NUMBER: US/10/366,493
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 10/075,869
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/653,182
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 4.0

```

; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pep 20
US-10-366-493-26

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 4 AKK 6

RESULT 52

US-10-285-394-292
; Sequence 292, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: FASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 292
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-292

Query Match 27.3%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
|||
Db 8 EKP 10

RESULT 53

US-10-264-309-93
; Sequence 93, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.

; APPLICANT: HERATH, HERATH
 ; APPLICANT: KIMMEL, LIDA H.
 ; APPLICANT: PAREKH, RAJESH B.
 ; APPLICANT: POTTER, DAVID M.
 ; APPLICANT: ROHLFF, CHRISTIAN
 ; APPLICANT: SILBER, B. MICHAEL
 ; APPLICANT: SNYDER, PETER J.
 ; APPLICANT: SOARES, HOLLY D.
 ; APPLICANT: STIGER, THOMAS R.
 ; APPLICANT: SUNDERLAND, P. TREY
 ; APPLICANT: TOWNSEND, ROBERT R.
 ; APPLICANT: WHITE, W. FROST
 ; APPLICANT: WILLIAMS, STEPHEN A.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
 ; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
 ; FILE REFERENCE: POA-002.01
 ; CURRENT APPLICATION NUMBER: US/10/264,309
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: 60/326,708
 ; PRIOR FILING DATE: 2001-10-03
 ; NUMBER OF SEQ ID NOS: 491
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 93
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-264-309-93

Query Match 27.3%; Score 3; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
 |||
 Db 1 EKP 3

RESULT 54

US-08-859-699-10

; Sequence 10, Application US/08859699A
 ; Publication No. US20010007017A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VELJKOVIC, Veljko
 ; APPLICANT: METLAS, Radmila
 ; TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE
 ; TITLE OF INVENTION: PROGNOSTIC MARKER FOR HIV DISEASE PROGRESSION
 ; FILE REFERENCE: VELJKOVIC et al. 08/859,699
 ; CURRENT APPLICATION NUMBER: US/08/859,699A
 ; CURRENT FILING DATE: 1997-05-21
 ; EARLIER APPLICATION NUMBER: GB 9610673.7
 ; EARLIER FILING DATE: 1996-05-22
 ; EARLIER APPLICATION NUMBER: GB 9623340.8
 ; EARLIER FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Derivative of
; OTHER INFORMATION: NTM peptide.
US-08-859-699-10

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 7 KE 8

RESULT 55

US-08-450-842-45

; Sequence 45, Application US/08450842
; Publication No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-842-45

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 56

US-08-891-525-2
; Sequence 2, Application US/08891525
; Publication No. US20020081643A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xiaodong
; APPLICANT: Liu, Xuesong
; TITLE OF INVENTION: Regulation of Apoptosis and In Vitro
; TITLE OF INVENTION: Model for Studies Thereof
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,525
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,268
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 45-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal

US-08-891-525-2

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 3 PN 4

RESULT 57

US-08-452-843A-15

; Sequence 15, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452,843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53, 127-137

US-08-452-843A-15

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 5 NK 6

RESULT 58

US-08-841-636A-28

; Sequence 28, Application US/08841636A
; Publication No. US20020168751A1

; GENERAL INFORMATION:
; APPLICANT: Miettinen-Oinonen, Arja
; APPLICANT: Londesborough, John
; APPLICANT: Vehmaanper , Jari
; APPLICANT: Haakana, Heli
; APPLICANT: M ntyl , Arja
; APPLICANT: Lantto, Raija
; APPLICANT: Elovainio, Minna
; APPLICANT: Joutsjoki, Vesa
; APPLICANT: Paloheimo, Marja
; APPLICANT: Suominen, Pirkko
; TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,636A
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,335
; FILING DATE: 17-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,926
; FILING DATE: 04-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,840
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/732,181
; FILING DATE: 16-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00550
; FILING DATE: 17-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Timothy J. Shea, Jr.
; REGISTRATION NUMBER: 41,306
; REFERENCE/DOCKET NUMBER: 1716.0510005/MAC/TJS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Melanocarpus albomyces
; STRAIN: ALKO4237
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /label= No. US20020168751A1632
US-08-841-636A-28

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 10 NK 11

RESULT 59

US-08-464-363-27

; Sequence 27, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morvile, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-363-27

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 4 KE 5

RESULT 60

US-08-344-824-44

; Sequence 44, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600

; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-44

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 4 KE 5

RESULT 61

US-09-113-924-21

; Sequence 21, Application US/09113924
; Patent No. US20010007019A1
; GENERAL INFORMATION:
; APPLICANT: Brigstock, David R.
; APPLICANT: Harding, Paul H.
; TITLE OF INVENTION: HEPARIN BINDING GROWTH FACTOR.(HBGF)
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,924
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/908,526
; FILING DATE: 07-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A., Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08766/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-113-924-21

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 4 ND 5

RESULT 62

US-09-341-643-1

; Sequence 1, Application US/09341643
; Patent No. US20010007020A1
; GENERAL INFORMATION:
; APPLICANT: GERL, MARTIN
; TITLE OF INVENTION: ANTIBODIES THAT BIND TO THE NIDOGEN-BINDING DOMAIN OF
; TITLE OF INVENTION: LAMININ, THEIR PRODUCTION AND USE
; FILE REFERENCE: 02481.1626-00000
; CURRENT APPLICATION NUMBER: US/09/341,643
; CURRENT FILING DATE: 1999-07-15
; EARLIER APPLICATION NUMBER: PCT/EP97/07241
; EARLIER FILING DATE: 1997-12-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-643-1

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 5 PN 6

RESULT 63

US-09-778-231-1

; Sequence 1, Application US/09778231
; Patent No. US20010018188A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Heau-Shan
; APPLICANT: Chang, I-Nan
; APPLICANT: Wu, Tzong-Zeng
; APPLICANT: Liao, Ya-Ling
; APPLICANT: Hsiung, Sung-Sheng
; TITLE OF INVENTION: Method for Detection of Trimethylamine
; FILE REFERENCE: LEEL-1-16811
; CURRENT APPLICATION NUMBER: US/09/778,231

; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: R.O.C. 86117774
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 09/143,708
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-778-231-1

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 10 KE 11

RESULT 64

US-09-729-402-3

; Sequence 3, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993

```

;      ATTORNEY/AGENT INFORMATION:
;      NAME: No. US20010021379Aland, Greta E.
;      REGISTRATION NUMBER: 35,302
;      REFERENCE/DOCKET NUMBER: 27866/32793
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (312) 474-6300
;      TELEFAX: (312) 474-0448
;      TELEX: 25-3658
;      INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 11 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-729-402-3

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Query Match          18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KP 6
      ||
Db      2 KP 3

```

RESULT 65

US-09-827-949-21

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; Sequence 21, Application US/09827949
; Patent No. US20010021505A1
; GENERAL INFORMATION:
; APPLICANT: Morris, Stephan W.
; APPLICANT: Look, A. Thomas
; TITLE OF INVENTION: ALK Protein Tyrosine Kinase/Receptor and Ligands Thereof
; FILE REFERENCE: 0656.0400004
; CURRENT APPLICATION NUMBER: US/09/827,949
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/670,827
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 09/100,089
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 08/542,363
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: US 08/160,861
; PRIOR FILING DATE: 1993-12-03
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-949-21

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Query Match          18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

Qy 3 KE 4
 ||
Db 10 KE 11

RESULT 66

US-09-802-077-14

; Sequence 14, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-14

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
Db 6 KP 7

RESULT 67

US-09-802-077-15

; Sequence 15, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26

; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-15

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 68

US-09-802-077-33

; Sequence 33, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-33

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 6 KP 7

RESULT 69

US-09-802-077-34

; Sequence 34, Application US/09802077
 ; Patent No. US20010033842A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
 ; FILE REFERENCE: P0718P2C2US
 ; CURRENT APPLICATION NUMBER: US/09/802,077
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 08/405,617
 ; PRIOR FILING DATE: 1995-03-15
 ; PRIOR APPLICATION NUMBER: US 08/185,899
 ; PRIOR FILING DATE: 1994-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US92/06860
 ; PRIOR FILING DATE: 1992-08-14
 ; PRIOR APPLICATION NUMBER: US 07/879,495
 ; PRIOR FILING DATE: 1992-05-07
 ; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; NUMBER OF SEQ ID NOS: 64
 ; SEQ ID NO 34
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-802-077-34

Query Match 18.2%; Score 2; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 10 AK 11

RESULT 70

US-09-758-318-8

; Sequence 8, Application US/09758318
 ; Patent No. US20010034021A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Muller, Martin
 ; APPLICANT: Gissmann, Lutz
 ; TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
 ; TITLE OF INVENTION: E1 and E2
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,337
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 33,220
; REFERENCE/DOCKET NUMBER: 05552-1199-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-758-318-8

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Query Match          18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      10 ND 11
      ||
Db      9 ND 10

```

RESULT 71

US-09-802-096-14

```

; Sequence 14, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768

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; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-14

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 6 KP 7

RESULT 72

US-09-802-096-15
; Sequence 15, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-15

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 73

US-09-802-096-33

```

; Sequence 33, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as
amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-33

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Query Match          18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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```

Qy      5 KP 6
      ||
Db      6 KP 7

```

RESULT 74

US-09-802-096-34

```

; Sequence 34, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as
amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768

```

; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-34

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 75

US-09-850-373-1

; Sequence 1, Application US/09850373
; Patent No. US20010051605A1
; GENERAL INFORMATION:
; APPLICANT: Strayer, David S
; TITLE OF INVENTION: Epidermal Growth Factor Inhibitor
; FILE REFERENCE: JEFF-0226-DIV
; CURRENT APPLICATION NUMBER: US/09/850,373
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 08/530,340
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: PCT/US94/03675
; PRIOR FILING DATE: 1994-04-04
; PRIOR APPLICATION NUMBER: 08/041,774
; PRIOR FILING DATE: 1993-04-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An epidermal
; OTHER INFORMATION: growth factor inhibitor peptide
US-09-850-373-1

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
||
Db 7 EK 8

Search completed: April 8, 2004, 16:35:47
Job time : 30.3077 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-17
Perfect score: 11
Sequence: 1 AKKEKPNKPND 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result
No. Score Match Length DB ID Description

1	4	36.4	11	4	Q9H4H5	Q9h4h5	homo sapien
2	3	27.3	11	10	Q8RV30	Q8rv30	zea mays (m
3	2	18.2	11	2	Q9AIY6	Q9aiy6	carsonella
4	2	18.2	11	2	Q9R790	Q9r790	borrelia ga
5	2	18.2	11	2	Q9L4F7	Q9l4f7	bacillus ce
6	2	18.2	11	2	Q47606	Q47606	escherichia
7	2	18.2	11	2	Q9R4B1	Q9r4b1	streptococc
8	2	18.2	11	2	Q9S618	Q9s618	prochloroco
9	2	18.2	11	2	P96319	P96319	desulfovibr
10	2	18.2	11	2	Q9EUZ3	Q9euz3	escherichia
11	2	18.2	11	2	Q9K332	Q9k332	staphylococ
12	2	18.2	11	2	Q9RFZ2	Q9rfz2	mycoplasma
13	2	18.2	11	2	P95518	P95518	pasteurella
14	2	18.2	11	2	Q47604	Q47604	escherichia
15	2	18.2	11	2	Q47420	Q47420	escherichia
16	2	18.2	11	2	Q44090	Q44090	acholeplasm
17	2	18.2	11	2	Q56413	Q56413	escherichia
18	2	18.2	11	2	Q9R446	Q9r446	neisseria g
19	2	18.2	11	2	Q8GMU3	Q8gmu3	acinetobact
20	2	18.2	11	2	Q7X566	Q7x566	thermus the
21	2	18.2	11	3	Q9UR95	Q9ur95	pichia angu
22	2	18.2	11	4	O60761	O60761	homo sapien
23	2	18.2	11	4	Q9UCP5	Q9ucp5	homo sapien
24	2	18.2	11	5	Q9NL65	Q9nl65	ascaris suu
25	2	18.2	11	5	Q9TWX6	Q9twx6	manduca sex
26	2	18.2	11	5	Q86D32	Q86d32	trypanosoma
27	2	18.2	11	5	Q86D31	Q86d31	trypanosoma
28	2	18.2	11	5	Q95PX6	Q95px6	caenorhabdi
29	2	18.2	11	6	Q9TRW5	Q9trw5	bos taurus
30	2	18.2	11	7	O77872	O77872	oreochromis
31	2	18.2	11	7	O77873	O77873	oreochromis
32	2	18.2	11	7	O77871	O77871	oreochromis
33	2	18.2	11	9	Q38415	Q38415	bacteriopha
34	2	18.2	11	9	Q37925	Q37925	bacteriopha
35	2	18.2	11	10	O65901	O65901	leavenworth
36	2	18.2	11	10	Q39784	Q39784	gossypium h
37	2	18.2	11	10	Q04131	Q04131	lycopersico
38	2	18.2	11	11	Q9JLE6	Q9jle6	rattus norv
39	2	18.2	11	11	Q8R2J7	Q8r2j7	mesocricetu
40	2	18.2	11	13	Q9PS64	Q9ps64	gallus gall
41	2	18.2	11	13	Q90735	Q90735	gallus gall
42	2	18.2	11	13	Q8AX69	Q8ax69	oreochromis
43	2	18.2	11	13	Q8AX68	Q8ax68	oreochromis
44	2	18.2	11	13	Q800X7	Q800x7	chelydra se
45	2	18.2	11	13	Q7T285	Q7t285	geochelone
46	2	18.2	11	13	Q7T284	Q7t284	geochelone
47	2	18.2	11	13	Q7T283	Q7t283	geochelone
48	2	18.2	11	13	Q7SX72	Q7sx72	geochelone
49	2	18.2	11	13	Q7SX71	Q7sx71	geochelone
50	2	18.2	11	15	Q9DZ32	Q9dz32	human immun
51	2	18.2	11	16	Q9K7A4	Q9k7a4	bacillus ha
52	1	9.1	11	2	O68237	O68237	borrelia bu
53	1	9.1	11	2	Q48933	Q48933	mycobacteri
54	1	9.1	11	2	Q47451	Q47451	escherichia
55	1	9.1	11	2	Q9AIZ7	Q9aiz7	carsonella
56	1	9.1	11	2	Q8RKN1	Q8rkn1	escherichia
57	1	9.1	11	2	Q52526	Q52526	rhizobium s

58	1	9.1	11	2	Q8KHL0	Q8kh10	streptococc
59	1	9.1	11	2	Q47602	Q47602	escherichia
60	1	9.1	11	2	Q8L2T4	Q8l2t4	neisseria m
61	1	9.1	11	2	Q9S623	Q9s623	prochloroco
62	1	9.1	11	2	Q9R5P3	Q9r5p3	serratia ma
63	1	9.1	11	2	P77404	P77404	escherichia
64	1	9.1	11	2	Q9RQ60	Q9rq60	buchnera ap
65	1	9.1	11	2	Q93RM6	Q93rm6	staphylococ
66	1	9.1	11	2	Q47600	Q47600	escherichia
67	1	9.1	11	2	Q8RMI8	Q8rmi8	enterococcu
68	1	9.1	11	2	O87882	O87882	mycobacteri
69	1	9.1	11	2	Q8KTN1	Q8ktn1	candidatus
70	1	9.1	11	2	P71228	P71228	escherichia
71	1	9.1	11	2	Q93MI7	Q93mi7	escherichia
72	1	9.1	11	2	Q47345	Q47345	escherichia
73	1	9.1	11	2	Q9AIZ8	Q9aiz8	carsonella
74	1	9.1	11	2	Q8KRA1	Q8kra1	streptococc
75	1	9.1	11	2	Q47059	Q47059	escherichia
76	1	9.1	11	2	Q44237	Q44237	anabaena sp
77	1	9.1	11	2	Q9R872	Q9r872	escherichia
78	1	9.1	11	2	Q56972	Q56972	yersinia pe
79	1	9.1	11	2	Q91UY9	Q91uy9	escherichia
80	1	9.1	11	2	Q8GL24	Q8gl24	borrelia bu
81	1	9.1	11	2	Q8GL19	Q8gl19	borrelia bu
82	1	9.1	11	2	P83537	P83537	lactobacill
83	1	9.1	11	2	Q47567	Q47567	escherichia
84	1	9.1	11	2	Q9X9S6	Q9x9s6	streptomyce
85	1	9.1	11	2	Q47569	Q47569	escherichia
86	1	9.1	11	2	Q7WUL8	Q7wul8	pseudomonas
87	1	9.1	11	3	O42763	O42763	aspergillus
88	1	9.1	11	3	Q9HDR9	Q9hdr9	aspergillus
89	1	9.1	11	3	Q9HFN8	Q9hfn8	candida rug
90	1	9.1	11	3	O43131	O43131	aspergillus
91	1	9.1	11	3	Q9HDR8	Q9hdr8	aspergillus
92	1	9.1	11	3	Q9URG1	Q9urg1	neurospora
93	1	9.1	11	3	Q9HDS0	Q9hds0	aspergillus
94	1	9.1	11	3	Q9HDR7	Q9hdr7	aspergillus
95	1	9.1	11	3	O60005	O60005	aspergillus
96	1	9.1	11	3	O60007	O60007	emericella
97	1	9.1	11	3	O42762	O42762	aspergillus
98	1	9.1	11	3	O43130	O43130	aspergillus
99	1	9.1	11	3	O60192	O60192	aspergillus
100	1	9.1	11	3	Q9C1R7	Q9c1r7	saccharomyc

ALIGNMENTS

RESULT 1

Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.

AC Q9H4H5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal

DE domains containing protein) (Fragment).

GN DJ620E11.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Skuce C.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL031669; CAC17164.2; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 36.4%; Score 4; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKEK 5
 ||||
 Db 7 KKEK 10

RESULT 2

Q8RV30

ID Q8RV30 PRELIMINARY; PRT; 11 AA.
 AC Q8RV30;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Methionine adenosyltransferase 1-like protein (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Various strains;
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
 RA Morgante M., Rafalski J.A.;
 RT "SNP frequency, haplotype structure and linkage disequilibrium in
 elite maize inbred lines."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF486085; AAL85893.1; -.
 DR EMBL; AF486086; AAL85894.1; -.
 DR EMBL; AF486087; AAL85895.1; -.
 DR EMBL; AF486088; AAL85896.1; -.
 DR EMBL; AF486089; AAL85897.1; -.
 DR EMBL; AF486090; AAL85898.1; -.
 DR EMBL; AF486091; AAL85899.1; -.
 DR EMBL; AF486092; AAL85900.1; -.
 DR EMBL; AF486093; AAL85901.1; -.
 DR EMBL; AF486094; AAL85902.1; -.
 DR EMBL; AF486095; AAL85903.1; -.
 DR EMBL; AF486096; AAL85904.1; -.
 DR EMBL; AF486097; AAL85905.1; -.

DR EMBL; AF486098; AAL85906.1; -.
 DR EMBL; AF486099; AAL85907.1; -.
 DR EMBL; AF486100; AAL85908.1; -.
 DR EMBL; AF486101; AAL85909.1; -.
 DR EMBL; AF486102; AAL85910.1; -.
 DR EMBL; AF486104; AAL85911.1; -.
 DR EMBL; AF486105; AAL85912.1; -.
 DR EMBL; AF486106; AAL85913.1; -.
 DR EMBL; AF486107; AAL85914.1; -.
 DR EMBL; AF486108; AAL85915.1; -.
 DR EMBL; AF486109; AAL85916.1; -.
 DR EMBL; AF486110; AAL85917.1; -.
 DR EMBL; AF486111; AAL85918.1; -.
 DR EMBL; AF486112; AAL85919.1; -.
 DR EMBL; AF486113; AAL85920.1; -.
 DR EMBL; AF486114; AAL85921.1; -.
 DR EMBL; AF486115; AAL85922.1; -.
 DR EMBL; AF486116; AAL85923.1; -.
 DR EMBL; AF486117; AAL85924.1; -.
 DR EMBL; AF486118; AAL85925.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1183 MW; 448D42ED3B05B337 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKP 6
 |||
 Db 7 EKP 9

RESULT 3

Q9AIY6

ID Q9AIY6 PRELIMINARY; PRT; 11 AA.
 AC Q9AIY6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Tryptophanyl-tRNA synthetase (Fragment).
 GN TRPS.
 OS Carsonella ruddii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
 OX NCBI_TaxID=114186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336438; PubMed=10877784;
 RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
 RA Baumann P.;
 RT "Cospeciation of psyllids and their primary prokaryotic
 RT endosymbionts.";
 RL Appl. Environ. Microbiol. 66:2898-2905(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21125546; PubMed=11222582;

RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
 RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont."
 RL J. Bacteriol. 183:1853-1861(2001).
 DR EMBL; AF211138; AAK15388.1; -.
 DR GO; GO:0004812; F:tRNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1295 MW; 0CA993A5345B5720 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
 ||
 Db 7 NK 8

RESULT 4

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.
 AC Q9R790;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN OSPC.
 OS Borrelia garinii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G25;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene."
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93700; AAC45535.1; -.
 DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 2 KK 3

RESULT 5

Q9L4F7

ID Q9L4F7 PRELIMINARY; PRT; 11 AA.
AC Q9L4F7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
DE (Fragment).
GN PLCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14579 type strain;
RX MEDLINE=20055637; PubMed=10589720;
RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
RT "Sequence analysis of three Bacillus cereus loci under PicR-regulated
RT genes encoding degradative enzymes and enterotoxin."
RL Microbiology 145:3129-3138(1999).
DR EMBL; AJ243711; CAB69804.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 3 NK 4

RESULT 6

Q47606

ID Q47606 PRELIMINARY; PRT; 11 AA.
AC Q47606;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems."
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63622; AAA24562.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
||
Db 4 EK 5

RESULT 7

Q9R4B1

ID Q9R4B1 PRELIMINARY; PRT; 11 AA.
AC Q9R4B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BX protein (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE.
RX MEDLINE=95252678; PubMed=7734831;
RA Gerlach D., Gunther E., Kohler W., Vettermann S., Fleischer B.,
RA Schmidt K.H.;
RT "Isolation and characterization of a mitogen characteristic of group A
RT streptococci (Streptococcus pyogenes).";
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 282:67-
RL 82(1995).
SQ SEQUENCE 11 AA; 1216 MW; CE527287CAA455A2 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 6 ND 7

RESULT 8

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.

RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in *Prochlorococcus* populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanog. 43:1615-1630(1998).
 DR EMBL; AF070132; AAD20740.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 5 KK 6

RESULT 9

P96319

ID P96319 PRELIMINARY; PRT; 11 AA.
 AC P96319;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Coded portion of proteolysis tag (Fragment).
 OS *Desulfovibrio desulfuricans*.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=97128184; PubMed=8972778;
 RA Williams K.P., Bartel D.P.;
 RT "Phylogenetic analysis of tmRNA secondary structure."
 RL RNA 2:1306-1310(1996).
 DR EMBL; U68081; AAB48023.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1250 MW; 85776D58CB5ABB5A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
 ||
 Db 3 ND 4

RESULT 10

Q9EUZ3

ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.
 AC Q9EUZ3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Ribosome binding factor A (Fragment).

GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RA Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 RT IQ490.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 2 AK 3

RESULT 11

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.
 AC Q9K332;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Geh (Fragment).
 GN GEH.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RX MEDLINE=20187516; PubMed=10722640;
 RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
 RT "Identification of a new repetitive element in Staphylococcus
 RT aureus.";
 RL Infect. Immun. 68:2344-2348(2000).
 DR EMBL; AF195967; AAF60251.1; -.
 DR EMBL; AF195963; AAF60243.1; -.
 DR EMBL; AF195964; AAF60245.1; -.
 DR EMBL; AF195965; AAF60247.1; -.
 DR EMBL; AF195966; AAF60249.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT "Isolation and characterization of the integration host factor genes
 RT of *Pasteurella haemolytica*.";
 RL FEMS Microbiol. Lett. 146:181-188(1997).
 DR EMBL; U56139; AAC44845.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 8 AK 9

RESULT 14

Q47604

ID Q47604 PRELIMINARY; PRT; 11 AA.
 AC Q47604;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems.";
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63621; AAA24560.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1296 MW; 3039A71A34472AB7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
 ||
 Db 7 NK 8

RESULT 15

Q47420

ID Q47420 PRELIMINARY; PRT; 11 AA.
 AC Q47420;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ORF11 protein.

OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92041688; PubMed=1657895;
 RA Sharples G.J., Lloyd R.G.;
 RT "Resolution of Holliday junctions in Escherichia coli: Identification
 RT of the ruvC gene product as a 19-Kilodalton protein.";
 RL J. Bacteriol. 173:7711-7715(1991).
 DR EMBL; X59551; CAA42127.1; -.
 DR PIR; S19015; S19015.
 SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
 ||
 Db 4 AK 5

RESULT 16

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.
 AC Q44090;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical export segment (Fragment).
 OS Acholeplasma laidlawii.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Acholeplasma.
 OX NCBI_TaxID=2148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A-EF22;
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
 RT "Sequence regions from Acholeplasma laidlawii which restore export of
 RT beta-lactamase in Escherichia coli.";
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; Z22875; CAA80495.1; -.
 DR PIR; S33519; S33519.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
 ||
 Db 2 KK 3

RESULT 17

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.
 AC Q56413;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IS602L region DNA, 5' end (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Transposon Tn602;
 RX MEDLINE=87318208; PubMed=2819910;
 RA Stibitz S., Davies J.E.;
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats."
 RL Plasmid 17:202-209(1987).
 DR EMBL; M22735; AAA27464.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
 ||
 Db 1 AK 2

RESULT 18

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.
 AC Q9R446;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Carbamoyl-phosphate synthase subunit A (Fragment).
 GN CARA.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RX MEDLINE=95291461; PubMed=7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.;
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
 RT gonorrhoeae includes a large, variable intergenic sequence which is
 RT also present in other Neisseria species."
 RL Microbiology 141:0-0(0).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
 RT "Complexity of the variable sequence between the carbamoyl-phosphate
 RT synthase genes of Neisseria species.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF029363; AAC78453.1; -.
 DR EMBL; AF029362; AAC78452.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 8 AK 9

RESULT 19

Q8GMU3

ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
 AC Q8GMU3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative catalase isozyme (Fragment).
 GN KATA.
 OS Acinetobacter lwoffii.
 OG Plasmid pKLH202.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=28090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TC108;
 RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
 RA Nikiforov V.G.;
 RT "pKLH2-like aberrant transposons and possible mechanisms of their
 RT dissemination.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ250245; CAC80800.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 6 KK 7

RESULT 20

Q7X566

ID Q7X566 PRELIMINARY; PRT; 11 AA.
 AC Q7X566;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;
 RT "Characterization of a LysN, the 4th enzyme in lysine biosynthesis, in
 RT an extremely thermophilic bacterium, Thermus thermophilus HB27.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB097117; BAC76940.1; -.
 KW Hypothetical protein.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1073 MW; 39792C1E75B72EB8 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
 Db 9 KP 10

RESULT 21

Q9UR95

ID Q9UR95 PRELIMINARY; PRT; 11 AA.
 AC Q9UR95;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Heat shock protein 60 homolog (Fragment).
 OS Pichia angusta (Yeast) (Hansenula polymorpha).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4905;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93223840; PubMed=8096822;
 RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
 RA Harder W., Veenhuis M.;
 RT "Affinity purification of molecular chaperones of the yeast Hansenula
 RT polymorpha using immobilized denatured alcohol oxidase.";
 RL FEBS Lett. 321:32-36(1993).
 SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 3 KE 4

RESULT 22

O60761

ID O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsumi S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 10 KK 11

RESULT 23

Q9UCP5

ID Q9UCP5 PRELIMINARY; PRT; 11 AA.
AC Q9UCP5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Aggrecan core protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92235266; PubMed=1569188;
RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;
RL J. Clin. Invest. 89:1512-1516(1992).

DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR GO; GO:0001501; P:skeletal development; NAS.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
 Db 10 KP 11

RESULT 24

Q9NL65

ID Q9NL65 PRELIMINARY; PRT; 11 AA.
 AC Q9NL65;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE ASABF-delta (Fragment).
 GN ASABF-DELTA.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "Ascaris suum asabf-delta gene, exon 2."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB029815; BAA89496.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1187 MW; 8BADD0CD1EAB5861 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
 ||
 Db 8 EK 9

RESULT 25

Q9TWX6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
 AC Q9TWX6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
 DE (Fragment).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92134256; PubMed=1734862;
 RA Touhara K., Prestwich G.D.;
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
 RT binding protein.";
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 10 AK 11

RESULT 26

Q86D32

ID Q86D32 PRELIMINARY; PRT; 11 AA.
 AC Q86D32;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dm28c;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545075; AAP21903.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 9 KK 10

RESULT 27

Q86D31

ID Q86D31 PRELIMINARY; PRT; 11 AA.
 AC Q86D31;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sylvio X10;
 RX MEDLINE=22557728; PubMed=12670512;
 RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."
 RL Int. J. Parasitol. 33:269-279(2003).
 DR EMBL; AF545076; AAP21906.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 9 KK 10

RESULT 28

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.
 AC Q95PX6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ZK1236.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Favello A.;

RT "The sequence of C. elegans cosmid ZK1236.";
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L13200; AAL11108.1; -.
 DR WormPep; ZK1236.8; CE29629.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
 ||
 Db 8 KK 9

RESULT 29

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.
 AC Q9TRW5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 25 kDa protein P25, peptide F4 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91372400; PubMed=1909972;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
 RA Shiratsuchi A., Uchida T., Imahori K.;
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
 RL FEBS Lett. 289:37-43(1991).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
 ||
 Db 1 KE 2

RESULT 30

077872

ID 077872 PRELIMINARY; PRT; 11 AA.
AC 077872;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049981; AAC41320.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 8 KP 9

RESULT 31

077873

ID 077873 PRELIMINARY; PRT; 11 AA.
AC 077873;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).

DR EMBL; AF049982; AAC41321.1; -.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 8 KP 9

RESULT 32

O77871

ID O77871 PRELIMINARY; PRT; 11 AA.

AC O77871;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 1 (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;

OC Cichlidae; Oreochromis.

OX NCBI_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,

RA Figueroa F., Sultmann H., Klein J.;

RT "Linkage relationships and haplotype polymorphism among cichlid mhc

RT class II B loci.";

RL Genetics 149:1527-1537(1998).

DR EMBL; AF049980; AAC41319.1; -.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 8 KP 9

RESULT 33

Q38415

ID Q38415 PRELIMINARY; PRT; 11 AA.

AC Q38415;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Ant1 protein (Fragment).
 OS Bacteriophage P7.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P1-like viruses.
 OX NCBI_TaxID=10682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90335968; PubMed=1696181;
 RA Citron M., Schuster H.;
 RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs."
 RL Cell 62:591-598(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319637; PubMed=1620606;
 RA Citron M., Schuster H.;
 RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
 RT RNA."
 RL Nucleic Acids Res. 20:3085-3090(1992).
 DR EMBL; M35139; AAA32437.1; -.
 DR PIR; S42449; S42449.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 2 KK 3

RESULT 34

Q37925

ID Q37925 PRELIMINARY; PRT; 11 AA.
 AC Q37925;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Bacteriophage fr replicase (Fragment).
 OS Bacteriophage fr.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
 OC Levivirus.
 OX NCBI_TaxID=12017;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Berzin V.M., Griбанov V.A., Cielens I.E., Jansone I.V., Gren E.J.;
 RT "The nucleotide sequence of the regulatory region of phage fr
 RT replicase cistron."
 RL Bioorg. Khim. 7:306-308(1981).
 DR EMBL; M34834; AAA32193.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 35

O65901

ID O65901 PRELIMINARY; PRT; 11 AA.
AC O65901;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
GN PGIC.
OS Leavenworthia crassa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Leavenworthia.
OX NCBI_TaxID=70805;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. CR8919/CR15, and cv. CR8919/CD6;
RA Liu F., Charlesworth D., Kreitman M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF054493; AAC19033.1; -.
DR EMBL; AF054492; AAC19032.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1208 MW; 5026B3A4BDD87337 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
||
Db 1 EK 2

RESULT 36

Q39784

ID Q39784 PRELIMINARY; PRT; 11 AA.
AC Q39784;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Alcohol dehydrogenase 2b-2 (Fragment).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=Blue Tag Siokra;
RA Millar A.A., Dennis E.S.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U53705; AAA98988.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 37

Q04131

ID Q04131 PRELIMINARY; PRT; 11 AA.
AC Q04131;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pik-red; TISSUE=Pericarp;
RX MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RT "Wound regulated accumulation of specific transcripts in tomato fruit:
RT interactions with fruit development, ethylene and light."
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL; X59884; CAA42539.1; -.
DR PIR; S19775; S19775.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 38

Q9JLE6

ID Q9JLE6 PRELIMINARY; PRT; 11 AA.
AC Q9JLE6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Thioredoxin reductase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rundlof A.-K., Arner E.S.J.;
 RT "Genomic sequence of parts of the rat thioredoxin reductase 1 gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF189711; AAF26304.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1255 MW; 804D1A1E6DDAA325 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
 ||
 Db 2 ND 3

RESULT 39

Q8R2J7

ID Q8R2J7 PRELIMINARY; PRT; 11 AA.
 AC Q8R2J7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Microphthalmia-associated transcription factor (Fragment).
 GN MITF.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Graw J., Pretsch W., Loester I.;
 RT "Mutation in intron 6 of the hamster mitf gene leads to skipping of
 RT the subsequent exon and creates a dominant animal model for the human
 RT Waardenburg syndrome type II."
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ458439; CAD30263.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1532 MW; 69D76B515449D414 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
 ||

Db

9 ND 10

RESULT 40

Q9PS64

ID Q9PS64 PRELIMINARY; PRT; 11 AA.
AC Q9PS64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PDI-like 53 kDa polypeptide (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92084663; PubMed=1660884;
RA Bassuk J.A., Berg R.A.;
RT "A novel 53-kDa polypeptide from chicken embryo."
RL J. Biol. Chem. 266:23732-23738(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1294 MW; C26984A00AE9C9D6 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5
||
Db 8 EK 9

RESULT 41

Q90735

ID Q90735 PRELIMINARY; PRT; 11 AA.
AC Q90735;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-globin gene (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81208060; PubMed=6263308;
RA Day L.E., Hirst A.J., Lai E.C., Mace M.Jr., Woo S.L.C.;
RT "5' domain and nucleotide sequence of an adult chicken chromosomal
RT beta-globin gene."
RL Biochemistry 20:2091-2098(1981).
DR EMBL; V00378; CAA23677.1; -.
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1372 MW; 271C02021B1DC1B3 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EK 5

||

Db 8 EK 9

RESULT 42

Q8AX69

ID Q8AX69 PRELIMINARY; PRT; 11 AA.

AC Q8AX69;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Wilm's tumor 1-like protein (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

OC Cichlidae; Oreochromis.

OX NCBI_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RA Streelman J.T., Howe A.E., Kocher T.D.;

RT "Isolation and mapping of candidate genes for sex determination, color
and the craniofacial skeleton of cichlid fishes.";

RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF534550; AAN77179.1; -.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1267 MW; D957B249A1AB1EA6 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 1 KP 2

RESULT 43

Q8AX68

ID Q8AX68 PRELIMINARY; PRT; 11 AA.

AC Q8AX68;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Wilm's tumor 1-like protein (Fragment).

OS Oreochromis aureus (Israeli tilapia).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;

OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=47969;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Streelman J.T., Howe A.E., Kocher T.D.;
 RT "Isolation and mapping of candidate genes for sex determination, color
 RT and the craniofacial skeleton of cichlid fishes."
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF534551; AAN77180.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1267 MW; D957B249A1AB1EA6 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
 Db 1 KP 2

RESULT 44

Q800X7

ID Q800X7 PRELIMINARY; PRT; 11 AA.
 AC Q800X7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Vacuolar H-ATPase B subunit (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 OX NCBI_TaxID=134619;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21876906; PubMed=11882478;
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 RT protein family in the hypothalamus of the snapping turtle, Chelydra
 RT serpentina serpentina."
 RL Environ. Health Perspect. 110:269-275(2002).
 DR EMBL; AF469184; AAO48730.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1350 MW; 2FC8B6D0B5BAB417 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 9 AK 10

RESULT 45

Q7T285

ID Q7T285 PRELIMINARY; PRT; 11 AA.
 AC Q7T285;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Creatine kinase (Fragment).
 OS Geochelone carbonaria (Red-footed tortoise).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
 OX NCBI_TaxID=50047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=red;
 RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
 RT the Giant Galapagos Tortoise."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101746; AAM34549.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

 Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 KE 4
 ||
 Db 10 KE 11

RESULT 46

Q7T284
 ID Q7T284 PRELIMINARY; PRT; 11 AA.
 AC Q7T284;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Creatine kinase (Fragment).
 OS Geochelone denticulata (Yellow footed tortoise).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
 OX NCBI_TaxID=101697;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=yellow2;
 RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
 RT the Giant Galapagos Tortoise."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101747; AAM34550.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 10 KE 11

RESULT 47

Q7T283

ID Q7T283 PRELIMINARY; PRT; 11 AA.
AC Q7T283;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone pardalis (Leopard tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=55540;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=to;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise."
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY101748; AAM34551.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 10 KE 11

RESULT 48

Q7SX72

ID Q7SX72 PRELIMINARY; PRT; 11 AA.
AC Q7SX72;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone chilensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=106216;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=1864, and 8136;
 RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
 RT the Giant Galapagos Tortoise.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101744; AAM34547.1; -.
 DR EMBL; AY101745; AAM34548.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
 ||
 Db 10 KE 11

RESULT 49

Q7SX71
 ID Q7SX71 PRELIMINARY; PRT; 11 AA.
 AC Q7SX71;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Creatine kinase (Fragment).
 OS Geochelone nigra (Galapagos giant tortoise).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
 OX NCBI_TaxID=66189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AG01, CAZ22, CRU1, ESP1, LG, ME4, PB3, P244, PZ6, and VA935;
 RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
 RT the Giant Galapagos Tortoise.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101734; AAM34537.1; -.
 DR EMBL; AY101735; AAM34538.1; -.
 DR EMBL; AY101736; AAM34539.1; -.
 DR EMBL; AY101737; AAM34540.1; -.
 DR EMBL; AY101738; AAM34541.1; -.
 DR EMBL; AY101739; AAM34542.1; -.
 DR EMBL; AY101740; AAM34543.1; -.
 DR EMBL; AY101741; AAM34544.1; -.
 DR EMBL; AY101742; AAM34545.1; -.
 DR EMBL; AY101743; AAM34546.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
||
Db 10 KE 11

RESULT 50

Q9DZ32

ID Q9DZ32 PRELIMINARY; PRT; 11 AA.
AC Q9DZ32;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., DePasquale M.P., Kartsonis N., Hanna G.J.,
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
RT infection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292799; AAG25407.1; -.
KW Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 18.2%; Score 2; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 6 PN 7

RESULT 51

Q9K7A4

ID Q9K7A4 PRELIMINARY; PRT; 11 AA.
AC Q9K7A4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BH3464.
GN BH3464.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001518; BAB07183.1; -.
 DR PIR; H84082; H84082.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 11 AA; 1219 MW; 5F7D235CB7272B13 CRC64;

Query Match 18.2%; Score 2; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4
 ||
 Db 4 KE 5

RESULT 52

O68237

ID O68237 PRELIMINARY; PRT; 11 AA.
 AC O68237;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Plasmid cp32-4, possible partition proteins (Fragment).
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OG Plasmid cp32-4.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B31;
 RX MEDLINE=98361033; PubMed=9695920;
 RA Stevenson B., Casjens S., Rosa P.;
 RT "Evidence of past recombination events among the genes encoding the
 RT Erp antigens of *Borrelia burgdorferi*.";
 RL Microbiology 144:1869-1879(1998).
 DR EMBL; AF022481; AAC35449.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1237 MW; 50E3B714D45B5DD7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
 |
 Db 3 N 3

RESULT 53

Q48933

ID Q48933 PRELIMINARY; PRT; 11 AA.
 AC Q48933; P77701; Q48932;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Alkyl hydroperoxide reductase C (Fragment).
 GN AHPC.
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC35728, and ATCC35727;
 RA Zhang Y., Deretic V.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC35735;
 RX MEDLINE=96256622; PubMed=8655566;
 RA Dhandayuthapani S., Zhang Y., Deretic V.;
 RT "Oxidative stress response and its role in sensitivity to isoniazid in
 RT mycobacteria: characterization and inducibility of ahpC by peroxides in
 RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
 RT tuberculosis.";
 RL J. Bacteriol. 178:3641-3649(1996).
 DR EMBL; U58031; AAB00320.1; -.
 DR EMBL; U57979; AAA99830.1; -.
 DR EMBL; U57978; AAA99829.1; -.
 DR EMBL; U57762; AAB00317.1; -.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 2 P 2

RESULT 54

Q47451

ID Q47451 PRELIMINARY; PRT; 11 AA.
 AC Q47451;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Plasmid pRJ1004 DNA (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=pRJ1004;
RX MEDLINE=96130847; PubMed=8594334;
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;
RT "Molecular genetics and transport analysis of the copper-resistance
RT determinants (pco) from Escherichia coli plasmid pRJ1004.";
RL Mol. Microbiol. 17:1153-1166(1995).
DR EMBL; X83541; CAA58524.1; -.
DR PIR; S70166; S52252.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
|
Db 2 N 2

RESULT 55

Q9AIZ7

ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211132; AAK15377.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 7 K 7

RESULT 56

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.
AC Q8RKN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-9 (Fragment).
GN BLACTX-M-9.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=743-D;
RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,
RA Prats G.;
RT "A novel complex *sul1*-type integron in Escherichia coli carrying the
RT bla(CTX-M-9) gene."
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY092058; AAM15718.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 57

Q52526

ID Q52526 PRELIMINARY; PRT; 11 AA.
AC Q52526;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Megaplasmid SYM nodulation node (Fragment).
OS Rhizobium sp.
OG Plasmid SYM.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=391;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=41;
RA Rostas K., Kondorosi E., Horvath B., Simoncsits A., Kondorosi A.;
RT "Conservation of extended promoter regions of nodulation genes in

RT Rhizobium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1757-1761(1986).
 DR EMBL; M13289; AAB86797.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1233 MW; C966816205BB1736 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
 Db 6 E 6

RESULT 58

Q8KHL0

ID Q8KHL0 PRELIMINARY; PRT; 11 AA.
 AC Q8KHL0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Streptococcus gallolyticus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=53354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4-C11, and 4-G10; TRANSPOSON=Tn5382-like;
 RA Dahl K.H., Sundsfjord A.;
 RT "vanB2 operons linked to Tn5382-like elements in Streptococcus strains
 RT from veal calves."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY035710; AAL07295.1; -.
 DR EMBL; AY035711; AAL07297.1; -.
 KW Hypothetical protein.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1329 MW; 93207414D1EEAB5E CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 8 A 8

RESULT 59

Q47602

ID Q47602 PRELIMINARY; PRT; 11 AA.
 AC Q47602;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems."
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63620; AAA24558.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 4 D 4

RESULT 60

Q8L2T4

ID Q8L2T4 PRELIMINARY; PRT; 11 AA.
 AC Q8L2T4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Histidinol phosphatase (Fragment).
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=126E;
 RX MEDLINE=22051050; PubMed=12055303;
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of
 RT Lipooligosaccharide (LOS) in Neisseria Species."
 RL Microbiology 148:1833-1844(2002).
 DR EMBL; AF470685; AAM33538.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1273 MW; 01EC828D0AA72050 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |

Db 2 K 2

RESULT 61

Q9S623

ID Q9S623 PRELIMINARY; PRT; 11 AA.
AC Q9S623;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070168; AAD23221.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1153 MW; 5F551A5CB05866D3 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 4 K 4

RESULT 62

Q9R5P3

ID Q9R5P3 PRELIMINARY; PRT; 11 AA.
AC Q9R5P3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SM2=NUCLEASE (Fragment).
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134331; PubMed=1663739;
RA Bannikova G.E., Blagova E.V., Dementiev A.A., Morgunova E.Yu.,
RA Mikchailov A.M., Shlyapnikov S.V., Varlamov V.P., Vainshtein B.K.;
RT "Two isoforms of Serratia marcescens nuclease. Crystallization and
RT preliminary X-ray investigation of the enzyme."
RL Biochem. Int. 24:813-822(1991).
DR PIR; A27356; A27356.
FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1179 MW; 6DF18EE04AA045BB CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 1 D 1

RESULT 63

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.
AC P77404;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
GN HSDR.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97206151; PubMed=9157244;
RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;
RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
RT high homology to the phage P1 genome: implications for the evolution
RT and spread of DNA restriction systems.";
RL Mol. Microbiol. 23:729-736(1997).
DR EMBL; X98145; CAA66840.1; -.
DR EMBL; X98144; CAA66839.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 64

Q9RQ60

ID Q9RQ60 PRELIMINARY; PRT; 11 AA.
AC Q9RQ60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Acetohydroxy acid synthase small subunit (Fragment).
GN ILVH.
OS Buchnera aphidicola.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=10555290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions.";
 RL Mol. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AF129503; AAF13796.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1330 MW; 0E89EF1E2045B050 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 2 K 2

RESULT 65

Q93RM6

ID Q93RM6 PRELIMINARY; PRT; 11 AA.
 AC Q93RM6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Lipophilic protein affecting bacterial lysis and methicillin
 DE resistance (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SRM551;
 RA Maki H.;
 RT "Upstream region of 11m gene.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB000542; BAB62080.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1191 MW; 4AC763F4C2C72727 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 8 A 8

RESULT 66

Q47600

ID Q47600 PRELIMINARY; PRT; 11 AA.

AC Q47600;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems.";
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63619; AAA24556.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

 Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 11 D 11
 |
 Db 6 D 6

RESULT 67
 Q8RMI8
 ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
 AC Q8RMI8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ErmB (Fragment).
 GN ERMB.
 OS Enterococcus hirae.
 OG Plasmid pMKH1.
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
 RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
 RT poultry origin.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF493942; AAM18554.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

 Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 11 K 11

RESULT 68

O87882

ID O87882 PRELIMINARY; PRT; 11 AA.
AC O87882;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alkyl hydroperoxide reductase (Fragment).
GN AHPC.
OS Mycobacterium xenopi.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1789;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC19250;
RX MEDLINE=98406038; PubMed=9733688;
RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deretic V.;
RT "Oxidative stress response and characterization of the oxyR-ahpC and
RT furA-katG loci in Mycobacterium marinum."
RL J. Bacteriol. 180:4856-4864(1998).
DR EMBL; U43810; AAC61663.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1147 MW; 45458CE1787041A7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 69

Q8KTN1

ID Q8KTN1 PRELIMINARY; PRT; 11 AA.
AC Q8KTN1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Phosphoribosylpyrophosphate synthetase (Fragment).
GN PRS.
OS Candidatus Tremblaya princeps.
OC Bacteria; Proteobacteria; Betaproteobacteria; Candidatus Tremblaya.
OX NCBI_TaxID=189385;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22083449; PubMed=12088995;
RA Baumann L., Thao M.L., Hess J.M., Johnson M.W., Baumann P.;

RT "The Genetic Properties of the Primary Endosymbionts of Mealybugs
 RT Differ from Those of Other Endosymbionts of Plant Sap-Sucking
 RT Insects.";
 RL Appl. Environ. Microbiol. 68:3198-3205(2002).
 DR EMBL; AF481911; AAM76018.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1127 MW; 4C127758A8676727 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 10 K 10

RESULT 70

P71228

ID P71228 PRELIMINARY; PRT; 11 AA.
 AC P71228;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nitrate/nitrite sensor transmitter (Fragment).
 GN NARQ.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=92374842; PubMed=1508040;
 RA Chiang R.C., Cavicchioli R., Gunsalus R.P.;
 RT "Identification and characterization of narQ, a second nitrate sensor
 RT for nitrate-dependent gene regulation in Escherichia coli.";
 RL Mol. Microbiol. 6:1913-1923(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=97113461; PubMed=8955321;
 RA Cavicchioli R., Kolesnikow T., Chiang R.C., Gunsalus R.P.;
 RT "Characterization of the aegA locus of Escherichia coli: control of
 RT gene expression in response to anaerobiosis and nitrate.";
 RL J. Bacteriol. 178:6968-6974(1996).
 DR EMBL; L34011; AAB46943.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1200 MW; 52E1CFFCA2D77403 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 4 K 4

RESULT 71

Q93MI7

ID Q93MI7 PRELIMINARY; PRT; 11 AA.
 AC Q93MI7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adhesin (Fragment).
 GN IHA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CFT073;
 RA Stell A.L.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF401752; AAK94916.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1203 MW; 8E2817ECBDD731B1 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 7 A 7

RESULT 72

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.
 AC Q47345;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Leader peptide.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
 RT "Identification of two Escherichia coli K12 proteins which are induced
 RT in response to pollutant stress."
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 2-11 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=85134883; PubMed=6396419;
 RA Hudson G.S., Davidson B.E.;

RT "Nucleotide sequence and transcription of the phenylalanine and
RT tyrosine operons of Escherichia coli K12.";
RL J. Mol. Biol. 180:1023-1051(1984).
DR EMBL; Z70523; CAA94435.1; -.
SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
|
Db 3 N 3

RESULT 73

Q9AIZ8

ID Q9AIZ8 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211126; AAK15376.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1384 MW; 07A038324339C724 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 7 K 7

RESULT 74

Q8KRA1

ID Q8KRA1 PRELIMINARY; PRT; 11 AA.
 AC Q8KRA1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Streptococcus lutetiensis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=150055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5-F9; TRANSPOSON=Tn5382-like;
 RA Dahl K.H., Sundsfjord A.;
 RT "vanB2 operons linked to Tn5382-like elements in Streptococcus strains
 RT from veal calves."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY035709; AAL07293.1; -.
 KW Hypothetical protein.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1329 MW; 93207414D1EEAB5E CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 8 A 8

RESULT 75

Q47059

ID Q47059 PRELIMINARY; PRT; 11 AA.
 AC Q47059;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Acetyl ornithine deacetylase (Fragment).
 GN ARGE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064529; PubMed=6292860;
 RA Charlier D., Piette J., Glansdorff N.;
 RT "IS3 can function as a mobile promoter in E. coli."
 RL Nucleic Acids Res. 10:5935-5948(1982).
 DR EMBL; J01589; AAA23485.1; -.
 DR PIR; I41138; I41138.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1181 MW; 93F0429162C05731 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
|
Db 3 N 3

Search completed: April 8, 2004, 15:46:08
Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
(without alignments)
111.135 Million cell updates/sec

Title: US-09-787-443A-17
Perfect score: 11
Sequence: 1 AKKEKPNKPND 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	3	27.3	11	1	TKNA_RANRI P29207 rana ridibu
2	3	27.3	11	1	TKND_RANCA P22691 rana catesb
3	3	27.3	11	1	TKN_PHYFU P08615 physalaemus
4	2	18.2	11	1	ASL2_BACSE P83147 bacteroides
5	2	18.2	11	1	CSI5_BACSU P81095 bacillus su
6	2	18.2	11	1	EFG_CLOPA P81350 clostridium
7	2	18.2	11	1	FAR9_CALVO P41864 calliphora
8	2	18.2	11	1	HS70_PINPS P81672 pinus pinas
9	2	18.2	11	1	OAIF_SARBU P83518 sarcophaga
10	2	18.2	11	1	Q20A_COMTE P80464 comamonas t
11	2	18.2	11	1	TKN1_UPEIN P82026 uperoleia i
12	2	18.2	11	1	TKN1_UPERU P08612 uperoleia r
13	2	18.2	11	1	TKN2_PSEGU P42987 pseudophryn
14	2	18.2	11	1	TKN3_PSEGU P42988 pseudophryn
15	2	18.2	11	1	TKN4_PSEGU P42989 pseudophryn
16	2	18.2	11	1	TKN5_PSEGU P42990 pseudophryn
17	2	18.2	11	1	TKNA_GADMO P28498 gadus morhu

18	2	18.2	11	1	TKNA_HORSE	P01290	equus cabal
19	2	18.2	11	1	TKNA_ONCMY	P28499	oncorhynchu
20	2	18.2	11	1	TKNA_RANCA	P22688	rana catesb
21	2	18.2	11	1	TKNA_SCYCA	P41333	scyliorhinu
22	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
23	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
24	1	9.1	11	1	BPP3_BOTIN	P30423	bothrops in
25	1	9.1	11	1	BPP4_BOTIN	P30424	bothrops in
26	1	9.1	11	1	BPPB_AGKHA	P01021	agkistrodon
27	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
28	1	9.1	11	1	BRK_MEGFL	P12797	megascolia
29	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
30	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
31	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
32	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
33	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
34	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
35	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
36	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
37	1	9.1	11	1	COXA_CANFA	P99501	canis famil
38	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
39	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
40	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
41	1	9.1	11	1	ES1_RAT	P56571	rattus norv
42	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
43	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynchu
44	1	9.1	11	1	LPW_THETH	P05624	thermus the
45	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
46	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
47	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
48	1	9.1	11	1	MLG_THETS	P41989	theromyzon
49	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
50	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
51	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
52	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
53	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
54	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
55	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
56	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
57	1	9.1	11	1	RR2_CONAM	P42341	conopholis
58	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
59	1	9.1	11	1	RS30_ONCMY	P83328	oncorhynchu
60	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
61	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
62	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
63	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
64	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
65	1	9.1	11	1	TKN2_UPERU	P08616	uperoleia r
66	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
67	1	9.1	11	1	TKN_ELEMO	P01293	eledone mos
68	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
69	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien
70	1	9.1	11	1	UXB2_YEAST	P99013	saccharomyc

ALIGNMENTS

RESULT 1

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda."
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
 |||
 Db 1 KPN 3

RESULT 2

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;

RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KPN 7
 |||
 Db 1 KPN 3

RESULT 3

TKN_PHYFU
 ID TKN_PHYFU STANDARD; PRT; 11 AA.
 AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main

RT active polypeptide of the skin of *Physalaemus fuscumaculatus*.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PNK 8
 |||
 Db 4 PNK 6

RESULT 4

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
 AC P83147;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
 OS *Bacteroides stercoris*.
 OC Bacteria; Bacteroidetes; *Bacteroides* (class); Bacteroidales;
 OC Bacteroidaceae; *Bacteroides*.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.

KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
||
Db 6 ND 7

RESULT 5

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis."
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
||
Db 7 KP 8

RESULT 6

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSA.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 DR InterPro; IPR000795; EF_GTPbind.
 DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
 KW Elongation factor; Protein biosynthesis; GTP-binding.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EK 5
 ||
 Db 5 EK 6

RESULT 7

FAR9_CALVO
 ID FAR9_CALVO STANDARD; PRT; 11 AA.
 AC P41864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRFamide 9.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2

RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; I41978; I41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
 ||
 Db 6 ND 7

RESULT 8

HS70_PINPS

ID HS70_PINPS STANDARD; PRT; 11 AA.
 AC P81672;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Heat shock 70 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
 CC (spot N164) is: 5.4, its MW is: 73 kDa.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 KW ATP-binding; Heat shock; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ND 11
 ||
 Db 6 ND 7

RESULT 9

OAIF_SARBU

ID OAIF_SARBU STANDARD; PRT; 11 AA.
AC P83518;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenic ovaries of Neobellieria bullata."
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NK 8
||
Db 1 NK 2

RESULT 10

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.

RC STRAIN=63;
 RX MEDLINE=96035889; PubMed=7556204;
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 RT quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-
 CC 1,2-dihydroquinoline.
 CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
 CC 1(2H)-one + reduced acceptor.
 CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
 CC step.
 CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
 CC two gamma chains (Probable).
 DR PIR; S66606; S66606.
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 1 AK 2

RESULT 11

TKN1_UPEIN

ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.

CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
 ||
 Db 4 PN 5

RESULT 12

TKN1_UPERU

ID TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
||
Db 4 PN 5

RESULT 13

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
AC P42987;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-II (PG-KII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; C60409; C60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7

Db 2 PN 3

RESULT 14

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D60409; D60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
 11
Db 4 PN 5

RESULT 15

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.

AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SPI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; E60409; E60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
 ||
 Db 2 PN 3

RESULT 16

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.

AC P42990;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P-like peptide II (PG-SPII).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog *Pseudophryne guntheri*.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; F60409; F60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PN 7
 ||
 Db 2 PN 3

RESULT 17

TKNA_GADMO
 ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;

RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
 Db 1 KP 2

RESULT 18

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine."
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P."
 RL Neuropeptides 14:105-110(1989).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01558; SPHO.
DR PIR; A60654; A60654.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
Db 3 KP 4

RESULT 19

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout."
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23308; S23308.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6
 ||
 Db 1 KP 2

RESULT 20

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.
 AC P22688;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin A (RTK A).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine."
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine."
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A61033; A61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 1 KP 2

RESULT 21

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.

AC P41333;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Substance P.

OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;

OC Scyliorhinidae; Scyliorhinus.

OX NCBI_TaxID=7830;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=93292508; PubMed=7685693;

RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;

RT "Primary structures and biological activities of substance-P-related
peptides from the brain of the dogfish, Scyliorhinus canicula.";

RL Eur. J. Biochem. 214:469-474(1993).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S33300; S33300.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KP 6

||

Db 1 KP 2

RESULT 22

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.

AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Crinia-angiotensin II.
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana."
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 23

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from Bacteroides stercoris HJ-15."
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.

CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
 |
 Db 1 N 1

RESULT 24

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; C37196; C37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |

RESULT 25

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
 AC P30424;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6

Db 4 P 4

RESULT 26

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=242054;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii.";
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 8 K 8

RESULT 27

BPP_AGKHP
 ID BPP_AGKHP STANDARD; PRT; 11 AA.
 AC P04562;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydus halys
 OS pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydus.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=86177022; PubMed=3008123;
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
 RT "Structure-function studies on the bradykinin potentiating peptide
 RT from Chinese snake venom (Agkistrodon halys pallas).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; JC0002; XAVIBH.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 4 P 4

RESULT 28

BRK_MEGFL

ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascolia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons.";
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 29

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.
 AC P82087;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.1/2.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 30

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 31

CA31_LITCI
 ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 32
 CA32_LITCI
 ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; *Litoria*.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 3 D 3

RESULT 33

CA41_LITCI
 ID CA41_LITCI STANDARD; PRT; 11 AA.
 AC P82091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.1/4.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 3 D 3

RESULT 34

CA42_LITCI
ID CA42_LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 3 D 3

RESULT 35

CEP1_ACHFU
ID CEP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica."
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 7 P 7

RESULT 36

CORZ_PERAM
ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from

RT the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 CC in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
 |
 Db 11 N 11

RESULT 37
 COXA_CANFA
 ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro; IPR003204; Cyt_c_ox5A.
 DR Pfam; PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 6 E 6

RESULT 38

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins."
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; A59146; A59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 4 P 4

RESULT 39

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
AC P58849;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5b.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins."
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., Delacruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 4 P 4

RESULT 40

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of *Conus marmoreus*."
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD_RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 6 K 6

RESULT 41

ES1_RAT
 ID ES1_RAT STANDARD; PRT; 11 AA.
 AC P56571;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE ES1 protein, mitochondrial (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
 CC P2) is: 8.9, its MW is: 25 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
 KW Mitochondrion.
 FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 42

FAR6_PENMO

ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 1 D 1

RESULT 43

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Ladderlectin (Fragment).
 OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; *Oncorhynchus*.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=97293418; PubMed=9149391;
 RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
 RT "A rainbow trout lectin with multimeric structure."
 RL Comp. Biochem. Physiol. 116B:385-390(1997).
 CC -!- FUNCTION: Lectin that binds sepharose.
 CC -!- COFACTOR: Calcium is essential for sepharose binding.
 CC -!- SUBUNIT: Multimeric.
 KW Lectin; Calcium.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 44

LPW_THETH

ID LPW_THETH STANDARD; PRT; 11 AA.
 AC P05624;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL.
 OS *Thermus thermophilus*.
 OC Bacteria; *Deinococcus-Thermus*; *Deinococci*; *Thermales*; *Thermaceae*;
 OC *Thermus*.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RX MEDLINE=89000781; PubMed=2844259;
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
 RT "Molecular cloning and nucleotide sequence of *Thermus thermophilus*
 RT HB8 trpE and trpG."
 RL Biochim. Biophys. Acta 950:303-312(1988).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.

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DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 45

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.

AC P04428;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Leucosulfakinin-I (LSK-I).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophaea.

OX NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86315858; PubMed=3749893;

RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;

RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to

RT gastrin and cholecystokinin.";

RL Science 234:71-73(1986).

CC -!- FUNCTION: Change the frequency and amplitude of contractions of

CC the hngut. Inhibits muscle contraction of hindgut.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A01622; GMROL.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; 1.

KW Hormone; Amidation; Sulfation.

FT MOD_RES 6 6 SULFATION.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 46

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: Stimulates hindgut contractions.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 1 E 1

RESULT 47

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;

RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 2 K 2

RESULT 48

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94298944; PubMed=8026574;
 RA Salzet M., Wattez C., Bulet P., Malecha J.;
 RT "Isolation and structural characterization of a novel peptide related
 RT to gamma-melanocyte stimulating hormone from the brain of the leech
 RT Theromyzon tessulatum.";
 RL FEBS Lett. 348:102-106(1994).
 CC -!- SIMILARITY: Belongs to the POMC family.
 DR PIR; S45698; S45698.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 10 K 10

RESULT 49

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human),
 OS Rattus norvegicus (Rat),
 OS Bos taurus (Bovine),
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 RT from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 RT hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
 RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
 CC in the G2/mitosis transition.
 CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
 CC and was called head activator by the authors, because it induced
 CC head-specific growth and differentiation in this animal. It has
 CC been found in mammalian intestine and hypothalamus.
 DR PIR; A01427; YHRT.
 DR PIR; A93900; YHXA.E.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJFHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
|
Db 2 P 2

RESULT 50

NUHM_CANFA

ID NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG.
DR InterPro; IPR002023; Cmplx1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|

Db

2 A 2

RESULT 51

NXSN_PSETE

ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 RT cloning, expression and protein characterization."
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.1e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

|

Db 5 K 5

RESULT 52

PKC1_CARMO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
 AC P82684;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
 OS Carausius morosus (Indian stick insect).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
 OC Heteronemiidae; Carausius.
 OX NCBI_TaxID=7022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RA Predel R., Kellner R., Gaede G.;
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";
 RL Eur. J. Entomol. 96:275-278(1999).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 1 D 1

RESULT 53

PQQC_PSEFL

ID PQQC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
 DE biosynthesis protein C) (Fragment).
 GN PQQC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqC family.
 CC -----
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DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
DR HAMAP; MF_00654; -; 1.
KW PQQ biosynthesis.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 3 D 3

RESULT 54

PVK1_PERAM

ID PVK1_PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT perisymphathetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 55

RANC_RANPI

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
 CC family.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 3 P 3

RESULT 56

RE41_LITRU

ID RE41_LITRU STANDARD; PRT; 11 AA.
 AC P82074;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australin red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
 |
 Db 4 D 4

RESULT 57

RR2_CONAM
 ID RR2_CONAM STANDARD; PRT; 11 AA.
 AC P42341;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chloroplast 30S ribosomal protein S2 (Fragment).
 GN RPS2.
 OS Conopholis americana (Squawroot).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
 OX NCBI_TaxID=4179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92145776; PubMed=1723664;
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
 RT of photosynthesis in a lineage of parasitic plants.";
 RL Curr. Genet. 20:515-518(1991).
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
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DR EMBL; X64567; CAA45868.1; -.
 DR PIR; S32575; S32575.
 DR HAMAP; MF_00291; -; 1.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
 KW Ribosomal protein; Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
 Db 11 E 11

RESULT 58

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
 AC P13179;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein) (Fragment).
 GN L.
 OS Chandipura virus (strain I653514).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Vesiculovirus.
 OX NCBI_TaxID=11273;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89299473; PubMed=2741347;
 RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
 RA Banerjee A.K.;
 RT "Structure and expression of the glycoprotein gene of Chandipura
 RT virus."
 RL Virology 171:285-290(1989).
 CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
 CC NUCLEOCAPSID (N) PROTEIN.
 CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
 CC PARAMYXOVIRUSES.
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CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 D 11
|
Db 2 D 2

RESULT 59

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
GN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O., Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow
RT trout skin.";
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 60

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE (R.PvuI) (Fragment).
GN PVUIR.
OS *Proteus vulgaris*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Proteus*.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system."
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
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CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
|
Db 5 E 5

RESULT 61

TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerinin-1.

OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
 FT DISULFID 2 10
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 6 P 6

RESULT 62

TIN4_HOPTI

ID TIN4_HOPTI STANDARD; PRT; 11 AA.
 AC P82654;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tigerinin-4.
 OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
 OC Hoplobatrachus.
 OX NCBI_TaxID=103373;
 RN [1]
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Skin secretion;
 RX PubMed=11031261;
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
 RA Devi A.S., Nagaraj R., Sitaram N.;
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
 RT tigerina.";
 RL J. Biol. Chem. 276:2701-2707(2001).
 CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
 CC S.aureus, M.luteus, P.putida and S.cerevisiae.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 5 A 5

RESULT 63

TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins."
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
|
Db 4 N 4

RESULT 64

TKN1_PSEGU

ID TKN1_PSEGU STANDARD; PRT; 11 AA.

AC P42986;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-I (PG-KI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 2 P 2

RESULT 65

TKN2_UPERU

ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80223080; PubMed=7389029;
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
 RT "Physalaemin- and bombesin-like peptides in the skin of the
 RT Australian leptodactylid frog *Uperoleia rugosa*.";
 RL Chem. Pharm. Bull. 28:689-695(1980).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 2 A 2

RESULT 66

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6
 |
 Db 2 P 2

RESULT 67

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musky octopus) (Ozaena moschata), and
 OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 RT endecapeptide of the posterior salivary glands of Eledone.";
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01561; EOOC.
 DR PIR; B01561; EOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 P 6

|

Db 2 P 2

RESULT 68

UF05_MOUSE

ID UF05_MOUSE STANDARD; PRT; 11 AA.
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFa CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

|

Db 1 K 1

RESULT 69

ULAG_HUMAN

ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 34 kDa.
 DR SWISS-2DPAGE; P31933; HUMAN.
 DR Siena-2DPAGE; P31933; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 E 4
 |
 Db 5 E 5

RESULT 70

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
 AC P99013;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=X2180-1A;
 RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
 RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
 RL Submitted (AUG-1995) to Swiss-Prot.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.20, its MW is: 9.2 kDa.
 DR SWISS-2DPAGE; P99013; YEAST.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.1e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 7 A 7

Search completed: April 8, 2004, 15:47:22
Job time : 5.15385 secs

